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(without alignments) 530.147 Million cell updates/sec
                                                                                                                                                                      December 20, 2002, 15:16:49; Search time 7.30435 Seconds
                                                                                                                                                                                                                                                                                                                                         1 IVNGENAVPGSWPWQVSLQD......AMYTRVSKFSTWINQVMAYN 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ggn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

Ggn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

Ggn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

Ggn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

Ggn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

Ggn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

Ggn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

Ggn2_6/ptodata/1/pubpaa/PUBCOMB.pep:*

Ggn2_6/ptodata/1/pubpaa/PUBCOMB.pep:*

Ggn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*

Ggn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     106657 seqs, 16763532 residues
                                                                                                                                                                                                                                                                           US-09-856-319B-4_COPY_34_264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Published_Applications_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                     BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                       Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                     Scoring table:
                                                                                                                                                                                                                                                                                                                                                  Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Database
                                                                                                                                                                   Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

SUMMARIES

		æ				
Result No.	Score	Query Match	Query Match Length DB	DB	ID	Description
-	756	60 4	192	-	118-00-025-207-820	ANK OCH CONCUESCO
•)	2	1	1	000 000 000 000	ממליה מינים מינים מלינים
7	755.5	60.3	263	10	US-09-888-615-96	Sequence 96, Appl
m	464.5	37.1	251	0	US-09-961-721-4	Sequence 4, Appli
4	464.5	37.1	791	6	US-09-967-386-1	Sequence 1, Appli
'n	464.5	37.1	810	10	US-09-946-893-2	Sequence 2, Appl1
9	462	36.9	812	6	US-09-335-325-1	
7	462	36.9	812	10	US-09-788-142-1	
6 0	462	36.9	812	10	US-09-761-120-1	
6	462	36.9	812	10	US-09-873-676-81	81,
10	459.5	36.7	270	10	US-09-923-779-152	Sequence 152, App
11	457.5	36.5	249	6	US-09-961-721-5	Sequence 5, Appli
12	457.5	36.5	273	10	US-09-925-297-695	Sequence 695, App
13	455.5	36.4	453	6	US-09-978-295A-69	_
14	455.5	36.4	453	6	69-269-816-60-SD	Sequence 69, Appl
15	455.5	36.4	453	σ	US-09-978-192A-69	-
16	455.5	36.4	453	12	US-10-052-586-64	
17	455	36.3	248	10	US-09-925-301-1017	Sequence 1017, Ap
18	455	36.3	327	10	US-09-804-156-16	Sequence 16, Appl
19	455	36.3	327	10	US-09-946-633-8	Sequence 8, Appli

; Sequence 96, Application US/0988615

RESULT 2 US-09-888-615-96

3 Sequence 103, App	Sequence 2, Appl1	Sequence 6, Appli	Sequence 5, Appl1		Sequence 934,	Seguence 934,		Sequence 934	Sequence 932, A	Sequence 932	Sequence 932	Sequence 932		Sequence 895,	Seguence 895,	Sequence 14,	Sequence 895	Sequence 23, 1	Sequence 90,	Sequence 110,	Sequence 14,	Sequence 69,	8 Sequence 108,	Sequence 126,			
US-09-888-615-10	US-09-948-094-2	US-09-961-721-6	US-10-045-367A-5	US-09-910-151-6	US-10-012-896-934	US-09-759-143-93	US-09-780-669-93	US-09-822-827-934	US-10-012-896-932	US-09-759-143-93	US-09-780-669-93	US-09-822-827-93	US-10-012-896-895	US-09-759-143-89	US-09-780-669-89	US-09-879-792-14	US-09-822-827-895	US-09-981-353-23	US-09-888-615-90	US-09-888-615-11	US-09-910-071-14	US-09-820-893-69	US-09-820-893-108	US-09-870-759-126	US-09-988-975A-1	ALIGNMENTS	
10			6	10	6	10	2	10	σ	20	10	10	σ	10	10	10	10	σ	10								
454	34	226	22(226	39	39	39	39	49.	493	49	49	493	493	49	49	492	387	32(457	223	417	480	1169	28		
36.3	35.8		35.0	35.0	34.4	34.4	34.4	34.4	34.4	34.4	34.4	34.4	34.2	34.2	34.2	34.2	34.2	34.1	33.9	33.8	33.8	33.7	33.7	33.7	33.7		
2	448.5	438.5	438.5	438.5	430.5	430.5	430.5	430.5	430.5	430.5	430.5	430.5	428.5	428.5	428.5	428.5	428.5	427.5	424	423.5	423	422.5	422.5	422	421.5		
20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45		

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61 SNAEPVQVLSIARAITHPNWNANTMNNDLTLLKLASPARYTAQVSPVCLASTNEALPSGL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30 IVNGENAVLGSWPWQVSLQDSSGFHFCGGSLISQSWVVTAAHCNVSPGRHFVVLGEYDRS 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                  Sequence 529, Application US/09925297

Batent No. US20020081659A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA105

CURRENT APPLICATION NUMBER: US/09/925,297

CURRENT FILING DATE: 2001-08-10

PRIOR PILING DATE: 2000-03-08

PRIOR FILING DATE: 2000-03-08

PRIOR FILING DATE: 1999-03-12

WHERE OF SEQ ID NOSS: 928

SOFTWARE: PATENTIN UNSS: 928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60.4%; Score 756; DB 10; Length 1:
84.4%; Pred. No. 4.4e-62;
Live 16; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    150 TCVTTGWGRLSGVGNVTPAHLQQVALPLVTVNQCRQYWGS 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 TCVTTGWGRISGVGNVTPARLQQVVLPLVTVNQCRQYWGA 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 84.49
Matches 135; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Homo sapiens
US-09-925-297-529
RESULT 1
US-09-925-297-529
                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 529
LENGTH: 192
                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
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Sequence 2, Application US/09946893
Fatent No. US20020072494A1
GENERAL INFORMATION:
TITLE OF INVENTION: Materials and methods relating to endothelial cell growth
TITLE OF INVENTION: Inhibitors
FILE REFERENCE: Mewburn
CURRENT APPLICATION NUMBER: US/09/946,893
CURRENT FILING DATE: 2001-09-05
                                                                                                                             ---ITDAMICAGG-SGASSCQGDSGGPLVCQKGN---TWVLIGIVSWGTKNC-NIQAPAM 213
                                                                                                                                                                                                          58 DRSSNAEP-VQVLSIARAITHPNWNANTMNNDLTLLKLASPARYTAQVSPVCLASTNEAL 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117 PSGLTCVTTGWGRISGVGNVTPARLQQVVLPLVTVNQCRQY--WGARITDAMICAG--GS 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LGEYDRSSNAEPVQVLSIARA-ITHPNWNANTM-----NNDLTLLKLASPARYTAQ-VSP 106
                                                                                                   VCLASTNEALPSGLTCVTTGWGRISGVGNVTPARLQQVVLPLVTVNQCR---QYWGAR-- 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                622 -QEVNLEPHYQEIEVSRLFLEPT-----RKDIALLKLSSPAVITDKVIPACLPSPNYVV 674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 IVNGENAVPGSWPWQVSLQDNTGFHFCGGSLISPNWVVTAAHC---QVTPGRHFVVLGEY 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              173 GASSCQGDSGGPLVCQKGNTWVLIGIVSWGTKNCNIQAPAMYTRVSKFSTWINQVMAYN 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Henkin, Jack
TITLE OF INVENTION: ANTIANGIOGENIC POLYPEPTIDES AND METHODS
TITLE OF INVENTION: FOR INHIBITING ANGIOGENESIS
FILE REPERBENCE: 6738.US.02
CURRENT APPLICATION NUMBER: US/09/967,386
CURRENT FILING DATE: 2001-09-26
PRIOR FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FASISEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 791;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37.1%; Score 464.5; DB 9;
41.8%; Pred. No. 1e-34;
tive 29; Mismatches 93;
                                                                                                                                                                                                                                                                                                                                                                                           US-09-967-386-1; Sequence 1, Application US/09967386; Sequence 1, OS2002015992A1
; Patent No. US2002015992A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 41.89
Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Homo sapiens
US-09-967-386-1
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241 YTRVSSYLDWI 251
                                                                                                                                                                                                                                                                     214 YTRVSKFSTWI 224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14 IVNGEDAVPGSWPWQVSLQDKTGFHFCGGSLISEDWVVTAAHCGVRTS-DVVVAGEFDGG 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 IVNGENAVPGSWPWQVSLQDNTGFHFCGGSLISPNWVVTAAHCQVTPGRHFVVLGEYDRS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 PGSW--PWQVSLQDNTG----FHFCGGSLISPNWVVTAAHC----QVTPGRHF-----VV 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SGGPLVCQKGNTWVLIGIVSWGTKNCNIQAPAMYTRVSKFSTWINQVMAYN 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Meyers, Rachel A.
TITLE OF INVENTION: m32404, A NOVEL HUMAN TRYPSIN AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 10448-096001
CURRENT APPLICATION NUMBER: U5/09/961,721
CURRENT PILING DATE: 2001-09-24
PRIOR APPLICATION NUMBER: 60,235,023
PRIOR FILING DATE: 2000-09-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        60.3%; Score 755.5; DB 1 ilarity 58.4%; Pred. No. 7.3e-62; Conservative 35; Mismatches 60
            GENERAL INFORMATION:
APPLICANT: PLOWMAN, GREGORY
APPLICANT: WHYTE, DAVID
APPLICANT: CAENEBEEL, SEAN
APPLICANT: CHARYDCZAK, GLEN
APPLICANT: CHARYDCZAK, GLEN
APPLICANT: MANNING, GERARD
APPLICANT: MANNING, GERARD
APPLICANT: MANNING, GERARD
TITLE OF INVENTION: NOVEL PROTEASES
FILE REFERENCE: 038602/1214
CURRENT APPLICATION NUMBER: 02/09/888,615
CURRENT FILING DATE: 2001-06-26
PRIOR FILING DATE: 2000-06-26
NUMBER OF SEQ ID NOS: 150
SOFTWARE: PATENT VET. 2010
SEQ ID NO 96
LENGTH: 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Consensus sequence US-09-961-721-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/09961721
Patent No. US20020156005A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
US20020064856A1
                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Homo sapiens
US-09-888-615-96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 135; Conserv
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US-09-961-721-4
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Best Local S
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Matches
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                                                                                                                                                                                                                                                                                                                                  581 VVGGCVAHPHSWPWQVSLRTRFGMHFCGGTLISPEWVLTAAHCLEKSPRPSSYKVILGAH 640
                                                                                                                                                                                                                                                                                                                                                                             58 DRSSNAEP-VQVLSIARAITHPNWNANTMNNDLTLLKLASPARYTAQVSPVCLASTNEAL 116
                                                                                                                                                                                                                                                                                                                                                                                                    117 PSGLTCVTTGWGRISGVGNVTPARLQQVVLPLVTVNQCRQY--WGARITDAMICAG--GS 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 694 ADRTECFITGWGETQGTFGA--GLLKEAQLPVIENKVCNRYEFLNGRVQSTELCAGHLAG 751
                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                           1 IVNGENAVPGSWPWQVSLQDNTGFHFCGGSLISPNWVVTAAHC---QVTPGRHFVVLGEY 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            173 GASSCOGDSGGPLVCQKGNTWVLIGIVSWGTKNCNIQAPAMYTRVSKFSTWINQVMAYN 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      O'Reilly, Micheal
Cao, Yihai
Sim, B. Kim Lee
TITLE OF INVENTION: Angiostatin Fragments and Method of Use
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                Length 810;
                                                                                                                                                                                                            37.1%; Score 464.5; DB 10; Length 41.8%; Pred. No. 1e-34; Live 29; Mismatches 93; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U.S.
ZIP: 30303-1769
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Jones & Askew STREET: 191 Peachtree Street, 37th Floor CITY: Atlanta STATE: Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Warren, William L.
REGISTRATION NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 05213-0126
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-818-3799
TELEFAX: 404-818-3799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/612,788 FILING DATE: <UNKNOWN> ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/335,325
FILING DATE: 17-Jun-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: US 60/230,893
; PRIOR FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 810
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-946-893-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/09335355
Patent No. US20020164717A1
GENERAL INFORMATION:
APPLICANT: Folkman, M. Judah
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LENGTH: 812 amino acids
TYPE: amino acid
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                                                                                                                                                                                                            Query Match 37.1
Best Local Similarity 41.8
Matches 100; Conservative
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57 YDRSSNAEPVQVLSIARAITHPNWNANTMNNDLTLLKLASPARYTAQVSPVCLASTNEAL 116
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                                                                                                                                                                                                                                                                                  Gaps
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O'Really, Michael
TITLE O'Really, Machael
TITLE OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                  16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/788,142
FILING DATE: 16-Feb-2001
CLASSIFICATION: ANNOWN>
PRIOR APPLICATION: ANNOWN>
PROPLICATION NUMBER: US 08/866,735
FILING DATE: CURNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: Warren, William L.
REGISTRATION NUMBER: 36,714
RESPERENCE/DOCKET UNMBER: 36,714
                                                                                                                                                                                                                                    Length 812;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Jones & Askew, LLP
STREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta
STATE: Georgia
                                                                                                                                                                                                                                  36.9%; Score 462; DB 9;
41.0%; Pred. No. 1.8e-34;
tive 32; Mismatches 93
                                                                                            ORGANISM: Murine
IMMEDIATE SOURCE:
CLONE: Plasminogen
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (404) 818-3700
04) 818-3799
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 30303-1769
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 812 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-788-142-1
; Sequence 1, Application US/09788142
; Patent No. US20010029246A1
; GENERAL INFORMATION:
                                                N-terminal
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                                                                                                                                                                                                                                                                                98; Conservative
                        ANTI-SENSE: NO
FRAGMENT TYPE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                  Query Match
Best Local Similarity
HYPOTHETICAL:
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TITLE OF INVENTION: All displays that and Endostatin Binding Proteins and Methods of Use FILE REFERENCE: 05213-0378 (43170-259333)
CURRENT APPLICATION NUMBER: US/09/873.676
PRIOR APPLICATION NUMBER: US 60/209,065
PRIOR PLING DATE: 2000-06-02
PRIOR PLING DATE: 2000-06-02
PRIOR PELICATION NUMBER: US 60/289,387
PRIOR FILING DATE: 2001-05-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57 YDRSSNAEPVQVLSIARAITHPNWNANTMNNDLTLLKLASPARYTAQVSPVCLASTNEAL 116
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                                                                     1 IVNGENAVPGSWPWQVSLQDN-TGFHFCGGSLISPNWVVTAAHC---QVTPGRHFVVLGE 56
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Patent No. US30020076721A1

GENERAL INFORMATION:
APPLICANT: Pyle, Ruth A.
APPLICANT: Yu, Jiangchun
APPLICANT: Tu. Jiangchun
APPLICANT: Wu, Jiangchun
APPLICANT: CAIOS, Michael D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
FILE REFERENCE: 210121.553
CURRENT APPLICATION NUMBER: US/09/923,779
CURRENT FILING DATE: 2001-08-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36.9%; Score 462; DB 10; 41.0%; Pred. No. 1.8e-34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36.7%; Score 459.5;
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                      Sequence 81, Application US/09873676 Patent No. US20020077289A1
                                                                                                                                                                                                                                                                      APPLICANT: MacDonald, Nicholas J. APPLICANT: Sim, Kim L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin version 3.1 SEQ ID NO 81 LENGTH: 812
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Best Local Similarity 41.05
Matches 98; Conservative
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US-09-923-779-152
                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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LENGTH: 270
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APPLICANT: O'Reilly, Michael
TITLE OF INVENTION: Nucleic Ardis Encoding Kringle 1-5 Region Fragments of Plasminoge
FITLE REFERENCE: 05940-0151 (43171-252068)
CURRENT APPLICATION NUMBER: US/09/761,120
CURRENT APPLICATION NUMBER: 09/309,821
PRIOR APPLICATION NUMBER: 09/309,821
PRIOR FILING DATE: 1999-05-11
PRIOR FILING DATE: 1999-05-30
NUMBER OF SEQ ID NOS: 47
SOFTWARE: Patentin version 3.0
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                                                                                                                                                                                                                                                                                                                                                              173 GASSCQGDSGGPLVCQKGNTWVLIGIVSWGTKNCNIQAPAMYTRVSKFSTWINQVMAYN 231
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                                                                                                                                                                                                                                                                                                                     93; Indels
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                                                                                                                                                                                                                                                                      ch 36.9%; Score 462; DB 10; Similarity 41.0%; Pred. No. 1.8e-34; 98; Conservative 32; Mismatches 93;
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41.0%; Pred. No. 1.8e-34;
tive 32; Mismatches 93;
                                                                                                                                                                                 CLONE: Plasminogen
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/09761120 Patent No. US20020037847Al GENERAL INFORMATION:
                                                                                         FRAGMENT TYPE: N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Plasminogen US-09-761-120-1
                         protein
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Best Local Similarity 41.0%
Matches 98; Conservative
                                                                                                                                        ORGANISM: Murine
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
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ORGANISM: Murinae gen. sp.
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                                                                                                                                                          IMMEDIATE SOURCE:
                                                                                                                 ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                     ANTI-SENSE: NO
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US-09-761-120-1
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US-09-978-295A-69; Sequence 69, Application US/09978295A; Patent No. US20020156006A1
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Filvaroff, Ellen
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Best Local Similarity 42.3%
Matches 102; Conservative
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Desnoyers, Luc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Baker Kevin P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eaton, Dan
                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (28
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                                                                                                                                                 60 SSNAEPVQVLSIARA-ITHPNWNANTM-----NNDLTLLKLASPARYTAQ-VSPVCLAST 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             113 NEALPSGLTCVTTGWGRISGVGNVTPARLQQVVLPLVTVNQCR---QYWGAR----ITD 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSDLPVGTTCTVSGWGRRPTKNLGLSDTLQEVVVPVVSRETCRSAYEYGGTDDKVEFVTD 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AMICAGG-SGASSCQGDSGGPLVCQKGN---TWVLIGIVSWGTKNC-NIQAPAMYTRVSK 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             185 NMICAGALGGKDACQGDSGGPLVCSDGNRDGRWELVGIVSWGSYGCARGNKPGVYTRVSS 244
                                                                                                                        58 DRSSNAEPVQVLSI--ARAITHPNWNANTM--NNDLTLLKLASPARYTAQVSPVCLASTN 113
                                                                                                                                                                                                                   SGASSCQGDSGGPLVC-QKGNTWVLIGIVSWGTK-NCN-IQAPAMYTRVSKFSTWINQVM 228
                                                                                                                                                                                                                                                                                            208 YIRSGCNGDSGGPLNCPTEDGGWQVHGVTSFVSGFGCNFIWKPTVFTRVSAFIDMIEETI 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13 PWQVSLQDNTG----FHFCGGSLISPNWVVTAAHC----QVTPGRHF-----VVLGEYDR 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 PWQVSLQVRSGGGSRKHFCGGSLISENWVLTAAHCVSGAASAPASSVRVSLSVRLGEHNL 64
                                                                                      29 VVHGEDAVPYSWPWQVSLQYEKSGSFYHTCGGSLIAPDWVVTAGHCISRDLTYQVVLGEY 88
                                                    1 IVNGENAVPGSWPWQVSLQ-DNTG--FHFCGGSLISPNWVVTAAHCQVTPGRHFVVLGEY 57
                                                                                                                                                                                                EALPSGLTCVTTGWGRISGVGNVTPARLQQVVLPLVTVNQCRQ--YWGARITDAMICAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Meyers, Rachel A.
TITLE OF INVENTION: m32404, A NOVEL HUMAN TRYPSIN AND USES
TITLE OF INVENTION: THEREOF;
FILE REFERENCE: 10448-096001
CURRENT APPLICATION NUMBER: US/09/961,721 '
CURRENT FILING DATE: 2001-09-24
PRIOR PILING DATE: 2000-09-25
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 249
                  Indels
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44.1%; Pred. No. 1.1e-34;
11ve 25; Mismatches 79;
Best Local Similarity 42.3%; Pred. No. 7.8e-35; Matches 102; Conservative 38; Mismatches 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Consensus sequence US-09-961-721-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5, Application US/09961721
Patent No. US20020156005A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 44.1%
Matches 108; Conservative
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US-09-961-721-5
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RESULT 12

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LOCATION: (27)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: SITE
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; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-297-695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    211 YIRSGCNGDSGGPLNCPTEDGGWQVHGVTSFVSGFGCNFIWKPTVFTRVSAFIDWIEETI 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58 DRSSNAEPVQVLSI--ARAITHPNWNANTM--NNDLTLLKLASPARYTAQVSPVCLASTN 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      114 EALPSGLTCVTTGWGRISGVGNVTPARLQQVVLPLVTVNQCRQ--YWGARITDAMICAGG 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SGASSCQGDSGGPLVC-QKGNTWVLIGIVSWGTK-NCN-IQAPAMYTRVSKFSTWINQVM 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 IVNGENAVPGSWPWQVSLQ-DNTG--FHFCGGSLISPNWVVTAAHCQVTPGRHFVVLGEY 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36.5%; Score 457.5; DB 10; Length 273; 42.3%; Pred. No. 1.2e-34; ive 37; Mismatches 89; Indels 13;
Sequence 695, Application US/09925297

Patent No. US20020081659A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION:

CURRENT APPLICATION NUCLEIC ACIDS, Proteins and Antibodies
FILE REFERENCE: PA105

CURRENT APPLICATION NUMBER: US/09/925,297

CURRENT FILING DATE: 2001-08-10

PRIOR FILING DATE: 2000-03-08

PRIOR FILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 928

SOFTWARE: PATENTIN Ver. 2.0

SEQ ID NO 695

LENGTH: 273
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Gerritsen, Mary E
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Gao, Wei-Qiang
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AFFLLCTING DATE: 1998-04-23
APPLICATION NUMBER: 60/083742
THE TAME DATE: 1998-04-30
                                                                          FILING DATE: 1998-04-01
APPLICATION NUMBER: 60/080328
                                                                                                                                                                                                                                                                                           FILING DATE: 1998-04-08
APPLICATION NUMBER: 60/081195
FILING DATE: 1998-04-08
APPLICATION NUMBER: 60/081203
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APPLICATION NUMBER: 60/083496
                                                                                                              FILING DATE: 1998-04-01
APPLICATION NUMBER: 60/080333
                                                                                                                                                                                      FILING DATE: 1998-04-01
APPLICATION NUMBER: 60/081070
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APPLICATION NUMBER: 60/081229
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PPLICATION NUMBER: 60/082568
ILING DATE: 1998-04-21
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FILING DATE: 1998-04-27
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LICATION NUMBER: 60/083499
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APPLICATION NUMBER: 60/083558
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APPLICATION NUMBER: 60/084366
FILING DATE: 1998-05-05
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   FILING DATE: 1998-03-31
                                                                                                                                                  LING DATE: 1998-04-01
PLICATION NUMBER: 60/
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APPLICATION NUMBER: 6
                                     FILING DATE: 1998-03
APPLICATION NUMBER:
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FILING DATE: 1998-04
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PPLICATION NUMBER:
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APPLICATION NUMBER:
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LICATION NUMBER:
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE OF INVENTION: Acids Encoding the Same FILE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2630PLCII.

CURRENT APPLICATION NUMBER: US/09/978,295A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-11-03
PRIOR PLICATION NUMBER: 60/064249
PRIOR PLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/065311
PRIOR PLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/077641
APPLICATION NUMBER: 60/077641
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FILING DATE: 1998-03-20
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APPLICATION NUMBER: 60/079920
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APPLICATION NUMBER: 60/077450
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FILING DATE: 1998-03-11
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APPLICATION NUMBER: 60/078886
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APPLICATION NUMBER: 60/078936
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APPLICATION NUMBER: 60/079663
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APPLICATION NUMBER: 60/079728
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APPLICATION NUMBER: 60/079923
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APPLICATION NUMBER: 60/080105
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APPLICATION NUMBER: 60/080107
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APPLICATION NUMBER: 60/080165
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APPLICATION NUMBER: 60/079294
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APPLICATION NUMBER: 60/079664
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                                                                                                                                                                                                                    Tumas, Daniel
Williams, P. Mickey
Wood, William I.
                                                                                                                                                               Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
                                                                                     Kuo, Sophia S.
Napier, Mary A.
Pan, James;
Paoni, Nicholas F.
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                                                                          Kljavin, Ivar J
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TITLE OF INVENTIONS: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTIONS: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTIONS: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTIONS: Secreted and Transmembrane Polypeptides and COURRENT PALLE NURSHIONS: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTIONS: 12001-10-16
PRIOR PILING DATE: 2001-10-16
PRIOR PILING DATE: 1997-10-17
PRIOR PILING DATE: 1997-11-13
PRIOR PILING DATE: 1997-11-13
PRIOR PILING DATE: 1996-3-11-13
PRIOR PILING DATE: 1996-3-13
PRIOR P
                                                                                                                                 Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
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Williams, P. Mickey
Wood, William I.
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Shelton, David L.
Stewart, Timothy A.
                                                                          Gerritsen, Mary E.
Goddard, Audrey
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                                                      Gerber, Hanspeter
                                                                                                                                                                                                                                         Kljavin, Ivar J.
Kuo, Sophia S.
                                                                                                                                                                                                                                                                                           Napier, Mary A.
                              Gao, Wei-Qiang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 453;
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Best Local Similarity 37.9%; Pred. No. 3.4e-34;
Matches 89; Conservative 39; Mismatches 96
                                                                                                                                                                       PRIOR FILING DATE: 1998-05-07
PRIOR PELING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084540
PRIOR FLING DATE: 1998-05-07
PRIOR FILING DATE: 1998-05-07
PRIOR PELING DATE: 1998-05-07
PRIOR PELING DATE: 1998-05-07
PRIOR PELING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084627
PRIOR APPLICATION NUMBER: 60/084643
PRIOR PILING DATE: 1998-05-07
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PRIOR FILING DATE: 1998-05-07
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PRIOR PAPLICATION NUMBER: 60/085339
PRIOR PALLICATION NUMBER: 60/085339
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PRIOR APPLICATION NUMBER: 60/085700
PRIOR PELING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/08559
PRIOR APPLICATION NUMBER: 60/08559
PRIOR PELING DATE: 1998-05-15
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PRIOR FILING DATE: 1998-05-15
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APPLICATION NUMBER: 60/085704
FILING DATE: 1998-05-15
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APPLICATION NUMBER: 60/084639
FILING DATE: 1998-05-07
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FILING DATE: 1998-05-13
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FILING DATE: 1998-05-13
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Patent No. US20020169284A1
GENERAL INFORMATION:
                                                 PPLICATION NUMBER: 60/084441
ILING DATE: 1998-05-06
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APPLICATION NUMBER: 60/084414
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Filvaroff, Ellen
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Botstein, David
Desnoyers, Luc
Eaton, Dan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-978-697-69
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R APPLICATION NUMBER: 60/080327

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R APPLICATION NUMBER: 60/080328

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R APPLICATION NUMBER: 60/080334

R APPLICATION NUMBER: 60/08034

R APPLICATION NUMBER: 60/081070

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APPLICATION NUMBER: 60/081229
FILING DATE: 1998-04-09
APPLICATION NUMBER: 60/081955
FILING DATE: 1998-04-15
APPLICATION NUMBER: 60/081817
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APPLICATION UNDBER: 60/081838
FILING DATE: 1998-04-15
APPLICATION NUMBER: 60/082568
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APPLICATION NUMBER: 60/083496

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                                                                                                                 APPLICATION NUMBER: 60/080165
FILING DATE: 1998-03-31
APPLICATION NUMBER: 60/080194
FILING DATE: 1998-03-31
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APPLICATION NUMBER: 60/081819
FILING DATE: 1998-04-15
APPLICATION NUMBER: 60/081952
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PPLICATION NUMBER: 60/082569
ILING DATE: 1998-04-21
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PLICATION NUMBER: 60/083545
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APPLICATION NUMBER: 60/081195
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APPLICATION NUMBER: 60/081203
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APPLICATION NUMBER: 60/082700
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APPLICATION NUMBER: 60/083392
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APPLICATION NUMBER: 60/083495
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APPLICATION NUMBER: 60/083499
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APPLICATION NUMBER: 60/083558
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APPLICATION NUMBER: 60/083500
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PPLICATION NUMBER: 60/082704
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APPLICATION NUMBER: 60/082797
60/080105
                               FILING DATE: 1998-03-31
APPLICATION NUMBER: 60/080107
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Best Local Similarity 37.9%; Pred. No. 3.4e-34;
Matches 89; Conservative 39; Mismatches 96
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                   APPLICATION NUMBER: 60/084366
                                                                                                                                   FILING DATE: 1998-05-06
APPLICATION NUMBER: 60/084637
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FILING DATE: 1998-05-07
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APPLICATION NUMBER: 60/084627
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PRIOR APPLICATION NUMBER: 60/085700
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APPLICATION NUMBER: 60/085689
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FILING DATE: 1998-05-15
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APPLICANT: Ashkenazi, Avi APPLICANT: Baker Kevin P

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RELING DATE: 1998-04-01
APPLICATION NUMBER: 60/080328
RELING DATE: 1998-04-01
R FILING DATE: 1998-03-27
R APPLICATION NUMBER: 60/079920
R FILING DATE: 1998-03-30
R APPLICATION NUMBER: 60/079923
R FILING DATE: 1998-03-30
R APPLICATION NUMBER: 60/080105
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R FILING DATE: 1998-03-31
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REILING DATE: 1998-04-21
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APPLICATION NUMBER: 60/081955
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APPLICATION NUMBER: 60/081819
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FILING DATE: 1998-04-08
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INDELICATION UNMBER: 60/081203
ILLING DATE: 1998-04-09
IPPLICATION NUMBER: 60/081229
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FILING DATE: 1998-04-29
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FILING DATE: 1998-03-31
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FILING DATE: 1998-03-31
APPLICATION NUMBER: 60/080327
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FILING DATE: 1998-04-08
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
IITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FITLE OF INVENTION: Acids Encoding the Same
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CURRENT FILING DATE: 2001-10-15
PRIOR PAPLICATION NUMBER: US/9918585
PRIOR FILING DATE: 2001-07-30
PRIOR PILING DATE: 1097-10-17
PRIOR APPLICATION NUMBER: 60/06429
PRIOR FILING DATE: 1997-11-03
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/06534
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1999-11-21
PRIOR PELING DATE: 1998-03-10
PRIOR PELING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077451
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
                                                                                                               Gao, Wei-Oiang
Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
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R APPLICATION NUMBER: 60/07791

R PILING DATE: 1998-03-12

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R APPLICATION NUMBER: 60/078910
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R APPLICATION NUMBER: 60/079294
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R APPLICATION NUMBER: 60/079656
R FILING DATE: 1998-03-26
R APPLICATION NUMBER: 60/079664
R FILING DATE: 1998-03-27
R RELIGATION NUMBER: 60/079689
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APPLICATION NUMBER: 60/079728
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                                                                                                                                                                                                                                                                                                                                   Pan, James;
Paoni, Nicholas F.
Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
                                                        Ferrara, Napoleon
Filvaroff, Ellen
                                                                                                                                                                                                                                                          Hillan, Kenneth J
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Kuo, Sophia S.
Napier, Mary A.
                                                                                                 ong, Sherman
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Best Local Similarity 37.9%; Pred. No. 3.4e-34;
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5200340-6 US-08-469-486-54 US-08-469-688-54 US-09-131-995-1 US-09-132-184-1 US-07-854-603-2 US-09-132-184-1 US-09-132-184-1 US-09-134-105-29 US-09-134-184-1 US-08-2034-0616-2 US-08-204-481-58 US-09-386-642-11 US-08-451-933-1 US-08-451-933-1 US-08-452-266-1
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ALIGNMENTS

RESULT 1 US-09-027-337-6 US-09-027-337-6 SEQUENCE 6. Application US/09027337B Datent No. 5972616 GENERAL INFORMATION: APPLICANT: Taninoto, Hiotoby J. APPLICANT: Taninoto, Hiotoby J. APPLICANT: Taninoto, Hiotoby J. TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease Overexpressed in TITLE OF INVENTION: Breast and Ovarian Carcinomas TITLE OF INVENTION: Breast and Ovarian Carcinomas TITLE OF INVENTION: Breast and Ovarian Carcinomas CURRENT APPLICANTON NUMBER: US/09/027,337B CURRENT FILING DATE: 1998-02-20 UNUMBER OF SEQ ID NOS: 13 CURRENT FILING DATE: 1998-02-20 ORGANISM: Unknown FEATURE: OUTHER INFORMATION: benologous to similar domain in TADG-15 OUS-09-027-337-6 OUGLY MATCh Best Local Similarity 56.8%: Pred: No. 5e-53; MATCHES INSTRUMENOVALODSSGFHFCGGSLISOSWVVTAAHCNVSPGRHFVVLGEYDR 92	09 93 SSNAEPLQVLSVSRAITHPSWNSTTMNNDYTLLKLASPAQYTRISPVCLASSNEALTEG 152
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APPLICATION NUMBER:
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US-08-557-146-13
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APPLICANT: STEMART, KENT D.
APPLICANT: STROUPE, STEVEN D.
TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS
TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
TITLE OF INVENTION: OF THE PROSTATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33 RIVNGENAVLGSWPWQVSLQDSSGFHFCGGSLISQSWVVTAAHCNVSPGRHFVVLGEYDR 92
TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease TITLE OF INVENTION: Overexpressed in Carcinomas Pries Reference: D6064CIP/D CURRENT APPLICATION WIDDER: US/09/644,600 CURRENT FILING DATE: 2000-08-23 PRIOR APPLICATION NUMBER: 09/421,213 PRIOR APPLICATION NUMBER: 09/421,213 PRIOR FILING DATE: 1999-10-20 PRIOR FILING DATE: 1998-02-20 NUMBER OF SEQ ID NOS: 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50.9%; Score 621.5; DB 4; 56.8%; Pred. No. 5e-53; tive 31; Mismatches 54;
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SOFTWARE: FastSRO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,483
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100 Abbott Park Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COLPITTS, TRACEY L. FRIEDMAN, PAULA N. GRANADOS, EDWARD N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; CTHER INFORMATION: Chymotrypsin US-09-644-600-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180 DSGGPLVCQKDGAWTLVGI 198
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Best Local Similarity 56.8%
Matches 113; Conservative
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CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 60064-3500
COMPUTER READABLE FORM:
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STREET: 10
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APPLICANT:
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APPLICANT:
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LENGTH: 231
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SNAEPLQVLSVSRAITHPSWNSTTMNNDVTLLKLASPAQYTTRISPVCLASSNEALTEGL 153
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APPLICANT: Hansson, Lennart
TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
TITLE OF INVENTION: Enzyme (SCCE)
NUMBER OF SEQUENCES: 17
CORRESPONDENCE SIDERSS:
ADDRESSEE: White & Case, Patent Department
                                                                                                                                                                                                                                                                                                                                                                                                              Length 230;
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SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 50.5%; Score 616.5; DB 4; Best Local Similarity 56.6%; Pred. No. 1.5e-52; Matches 112; Conservative 31; Mismatches 54;
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NAME: Sterner, Richard J.
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-181
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELEPHONE: (212) 819-8783
TELEPHONE: (212) 354-8113
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14-DEC-1995
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COUNTRY: U.S.A.
ZIP: 10036-2787
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIALE
OPERATING SYSTEM: PC-DOS/MS-DX
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
                                                                      REFERENCE/DOCKET NUMBER: 61
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: No. 6232456e
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        214 SGGPLVCQKGNTWVLIGI 231
                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 230 amino acids
                                                                                                                                          TELEFAX: 847/938-2623
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                                                                                                                                                                                                                                                                      TYPE: amino acid STRANDEDNESS: Si
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; MOLECULE TYPE: polypeptide US-09-154-344-13
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Recombinant Stratum Corneum Chymotryptic
Enzyme (SCCE)
: 17
                                                                                                                                                      Length 229;
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APPLICATICN NUMBER: US/09/154,344
FILING DATE: 16-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Egelrud, Torbjorn
APPLICANT: Bellud, Lennart
TITLE OF INVENTION: Recombinant Stratum Corneum
TITLE OF INVENTION: Enzyme (SCCE)
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: White & Case, Patent Department
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                     h 49.9%; Score 609; DB 2; Similarity 57.1%; Pred. No. 8.2e-52; 13; Conservative 30; Mismatches 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/557,146
FILING DATE: 14-DEC-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 13, Application US/09154344
Patent No. 5981256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Sterner, Richard J.
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (212) 819-8783
TELEFAX: (212) 354-8113
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 229 amino acids
INFORMATION FOR SEQ ID NO: 13:
                              LENGTH: 229 amino acids
TYPE: amino acids
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SGGPLVCQKDGAWTLVGI 196
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                 SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acids
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: New York COUNTRY: U.S.A. ZIP: 10036-2787
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                                                                                                                                                     Query Match
Best Local Simi
Matches 113;
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                                                                                                                  US-08-557-146-13
                            LENGTH:
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                                                                                                                                                             94 SNAEPLOVLSVSRAITHPSWNSTTMNNDVTLLKLASPAQYTTRISPVCLASSNEALTEGL 153
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                                                                                                                                                                                                                                            154 TCVTTGWGRLSGVGNVTPAHLQQVALPLVTVNQCRQYWDSSITDSMICAGGAGASSCQGD
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  Length 229;
                                            Indels
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: PATENTIN BATA:
APPLICATION NUMBER: US/08/278,091
FILING DATE: 21.JUL-1994
CLASSIFICATION: 435
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; Pred. No. 1.1e-51;
36; Mismatches 49;
  Score 609; DB 2;
Pred. No. 8.2e-52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Sim & McBurney
Suite 701, 330 University Avenue
                                         30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 10, Application US/08278091 Patent No. 5506139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: LOOSMORE, Sheena M
APPLICANT: YANG, Yan-Ping
APPLICANT: CHONG, Pele
APPLICANT: CHONG, Raymond P.
APPLICANT: KLEIN, Michel H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 10.
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPRANE: (416) 595-1153
TELEPRAN: (416) 595-1163
INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS:
LENGTH: 228 amino acids
49.9%;
ilarity 57.1%;
Conservative 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 55.6%;
Matches 110; Conservative 3
                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                            214 SGGPLVCQKGNTWVLIGI 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: Canada
ZIP: M5G 1R7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: Ontario
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: Suite
CITY: Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-278-091-10
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                                         Matches 113;
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214
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                                                                         60 SSSEKIOKLKIAKVFKNSKYNSLTINNDITLLKLSTAASFSQTVSAVCLPSASDFAAGT 119
                                                      94 SNAEPLQVLSVSRAITHPSWNSTTMNNDVTLLKLASPAQYTTRISPVCLASSNEALTEGL 153
                                                                                                                           154 TCVTTGWGRLSGVGNVTPAHLQQVALPLVTVNQCRQYWDSSITDSMICAGGAGASSCQGD 213
                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34 IVNGENAVLGSWPWQVSLQDSSGFHFCGGSLISQSWVVTAAHCNVSPGRHFVVLGEYDRS 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Analog of Haemophilus Hin47 Protein with TITLE OF INVENTION: Reduced Protease Activity NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,859
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 607.5; DB
Pred. No. 1.1e-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Stewart, Michael I.
REGISTRATION NUMBER: 24,973
REGISTRATION NUMBER: 24,973
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
INFORMATION FOR SEO ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Sim & McBurney
Suite 701, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRICE APPLICATION DATA:
APPLICATION NUMBER: US 08/296,149
FILING DATE: 26-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/278,091
FILING DATE: 21-JUL-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                         Sequence 10, Application US/08483859
Fatent No. 5656436
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                 LOOSMORE, Sheena M
                                                                                                                                                                                                                                                                                                                                                                                                  YANG, Yan-Ping
CHONG, Pele
OOMEN, Raymond P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: OOMEN, Raymond P
APPLICANT: KLEIN, Michel H.
                                                                                                                                                                                                                     178 SGGPLVCKKNGAWTLVGI 195
                                                                                                                                                                                                  214 SGGPLVCQKGNTWVLIGI 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           228 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 55.64
Matches 110; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: Ontario
COUNTRY: Canada
21P: MSG 1F7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               single
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ADDRESSEE: Sim & MCB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: linear
US-08-483-859-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Toronto
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                                                                                                                                                                                                                                                                                       RESULT 7
US-08-483-859-10
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SNAEPLQVLSVSRAITHPSWNSTIMNNDVTLLKLASPAQYTTRISPVCLASSNEALTEGL 153
                            60 SSSEKIQKLKIAKVFKNSKYNSLTINNDITLLKLSTAASFSQTVSAVCLPSASDDFAAGT 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34 IVNGENAVLGSWPWQVSLQDSSGFHFCGGSLISQSWVVTAAHCNVSPGRHFVVLGEYDRS 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of Haemophilus Hin47 Protein with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,173
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 49.8%; Score 607.5; DB 1
Best Local Similarity 55.6%; Pred. No. 1.1e-51;
Matches 110; Conservative 36; Mismatches 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Analog of Haemophilus Hin-
TITLE OF INVENTION: Reduced Protease Activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S: Sim & McBurney
Suite 701, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/296,149
FILING DATE: 26-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/278,091
FILING DATE: 21-UL-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                         Sequence 10, Application US/08472173 Patent No. 5665353
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: LOOSMORE, Sheena M
APPLICANT: YANG, Yan-Ping
APPLICANT: CHONG, Pele
PPLICANT: OOMEN, RAYMOND P.
APPLICANT: KLEIN, Michel H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Stewart, Michael I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                 SGGPLVCQKGNTWVLIGI 231
                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
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CITY: Toronto
STATE: Ontario
COUNTRY: Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RY: Canada
M5G 1R7
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228 amino acids
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                                                                                 214 SGGPLVCQKGNTWVLIGI
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Matches 110; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear
US-08-482-816-10
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                                                                                                                                                               RESULT 10
US-08-482-816-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                STATE:
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213
                                                                  60 SSSEKIQKLKIAKVFKNSKYNSLTINNDITLLKLSTAASFSQTVSAVCLPSASDDFAAGT 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SNAEPLQVLSVSRAITHPSWNSTIMNNDVTLLKLASPAQYTTRISPVCLASSNEALTEGL 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCVTTGWGRLSGVGNVTPAHLQQVALPLVTVNQCRQYWDSSITDSMICAGGAGASSCQGD
                                                                                                                                                                                                                                                                                                                                                              of Haemophilus Hin47 Protein with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUSTWARE: PC-DOS/MS-DOS
SUSTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,167
FILING DATE: 07.3UN-1995
PRIOR APPLICATION: 435
PRIOR APPLICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
                                                                                                                                                                                                                                                                           APPLICANT: LOOSMORE, Sheena M.
APPLICANT: YANG, Yan-Ping
APPLICANT: CHONG, Pele
APPLICANT: CHONEN, Raymond P.
APPLICANT: OMEN, Raymond P.
APPLICANT: NEIN, Michel H.
TITLE OF INVENTION: Analog of Haemophilus Hin47
TITLE OF INVENTION: Reduced Protease Activity
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 49.8%; Score 607.5; DB 2; Best Local Similarity 55.6%; Pred. No. 1.1e-51; Matches 110; Conservative 36; Mismatches 49;
                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Sim 6 McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Stewart, Michael I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-508 MIS:vg
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION UNBER: US 08/296,149

FILING DATE: 26-AUG-1994

PRIOR APPLICATION UNBER: US 08/278,091

FILING DATE: 21-UL-1994

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                             Sequence 10, Application US/08487167
Patent No. 5869302
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (416) 595-1155
                                                                                                                                 SGGPLVCQKGNTWVLIGI 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 228 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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US-08-487-167-10
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GENERAL INFORMATION:
APPLICANT: LOOSMORE, Sheena M
APPLICANT: Yan-Grid And APPLICANT: Yan-Grid APPLICANT: APPLICANT: OWEN, Raymond P.
APPLICANT: CLOSMOR, Raymond P.
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: Analog of Haemophilus Hin47 Protein with Reduced Protease A
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .,
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TCVTTGWGRLSGVGNVTPAHLQQVALPLVTVNQCRQYWDSSITDSMICAGGAGASSCQGD 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 228;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .1e-51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1038-494 MIS:vg
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55.6%; Pred. No. 1.1e
tive 36; Mismatches
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APPLICATION NUMBER: US 08/296,149
FILING DATE: 26-AGG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/278,091
FILING DATE: 21-JUL-1994
ATTORNEY, AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, v CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,816
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                            Sequence 10, Application US/08482816
Patent No. 5935573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 10:
                                                                                           178 SGGPLVCKKNGAWTLVGI 195
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Sequence 10, Application US/08801499 Patent No. 5962430
                                                     GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY:
US-08-801-499-10
                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                     STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120 TCVTTGWG-LTRYAN-TPDRLQQASLPLLSNTNCKKYWGTKIKDAMICAGASGVSSCMGD 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34 IVNGENAVLGSWPWQVSLQDSSGFHFCGGSLISQSWVVTAAHCNVSPGRHFVVLGEYDRS 93
                                                                                                                                                                                                                                                                                                  Analog of Haemophilus Hin47 Protein with
Reduced Protease Activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 228;
                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/296,149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                           Suite 701, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36; Mismatches
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49.8%; Score 607.5;
Best Local Similarity 55.6%; Pred. No. 1.1
Matches 110; Conservative 36; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTATION NUMBER: 24,973
REFERNCE/DOCKET NUMBER: 1038-390
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416, 595-1155
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 228 amino acids
                                                                                                                                                         Sequence 10, Application US/08296149
Patent No. 5939297
GENERAL INFORMATION:
APPLICANT: LOOSMORE, Sheena M
                                                                                                                                                                                                                              APPLICANT: YANG, Yan-Ping
APPLICANT: CHONG, Pele
PELICANT: COMEN, Raymond P.
APPLICANT: KLEIN, MICHEL H.
                                                                                                                                                                                                                                                                                                                                                                              Sim & McBurney
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                                                       214 SGGPLVCQKGNTWVLIGI 231
                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Ana-
TITLE OF INVENTION: Red
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: SIM & MCBU:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 514
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                                                                                                                                                                                                                                                                                                                                                                                    STREET: Surc
                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Ontario
COUNTRY: Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                      RESULT 11
US-08-296-149-10
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APPLICANT: LOOSMORE, Sheena M
APPLICANT: YANG, Yan-Ping
APPLICANT: OMEN, Raymond P.
APPLICANT: COMEN, Raymond P.
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: Analog of Haemophilus Hin47 Protein with Reduced Protease A
NUMBER OF SEQUENCES: 23
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                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/801,499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 49.8%; Score 607.5; DB 2; Best Local Similarity 55.6%; Pred. No. 1.1e-51; Matches 110; Conservative 36; Mismatches 49;
                                                                                                                                                                                          ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
CITY: Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1038-671 MIS: jb
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/482,816
FILING DATE: 07-UUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US 08/296,149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Stewart, Michael I
REGISTATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1151
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 26-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
FILING DATE: 21-JUL-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SGGPLVCQKGNTWVLIGI 231
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LENGTH: 228 amino acids
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: single
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                                                                                                                                                                    CORRESPONDENCE ADDRESS
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60 SSSEKIOKLKIAKVFKNSKYNSLTINNDITLLKLSTAASFSQTVSAVCLPSASDFAAGT 119
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APPLICANT: KLEIN, Michel H.

TITLE OF INVENTION: Analog of Haemophilus Hin47 Protein with
TITLE OF INVENTION: Reduced Protease Activity
NUMBER OF SEQUENCES: 23
CORRESPENDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49.8%; Score 607.5; DB 3; Length 228; 55.6%; Pred. No. 1.1e-51;
                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/074,660
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/487,167
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/296,149
FILING DATE: 26-4UG-1994
PRIOR APPLICATION NUMBER: US 08/278,091
FILING DATE: 21-JUL-1994
ATTORNEY AGENT INFORMATION:
NAME: Stewart, Michael I.
REGISTRATION NUMBER: 24,933
REFERENCE/DOCKET NUMBER: 1938-731 MIS: Jb
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36; Mismatches
                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 6025342
GENERAL INFORMATION:
APPLICANT: LOOSMORE, Sheena M.
APPLICANT: YANG, Yan-Ping
APPLICANT: CHONG, Pele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          214 SGGPLVCQKGNTWVLIGI 231
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amino acid
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                                                                                                                                                                                         STATE: Ontario
COUNTRY: Canada
ZIP: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single
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Matches 110; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34 IVNGENAVLGSWPWQVSLQDSSGFHFCGGSLISQSWVVTAAHCNVSPGRHFVVLGEYDRS 93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                    APPLICANT: LOOSMORE, Sheena M.
APPLICANT: YANG, Yan-Ping
APPLICANT: CHONG, Pele
APPLICANT: CHONG, Pele
APPLICANT: CHONG, Pele
APPLICANT: Michel H.
APPLICANT: KLEIN, Michel H.
APPLICANT: RIBIN, Michel H.
APPLICANT: RIBIN, MICHEL H.
APPLICANT: RIBIN, MICHEL H.
APPLICANT: MICHEL SAMALOG OF HAEMOPHILUS HIN47 WITH REDUCED TITLE OF INVENTION: PROTEASE ACTIVITY
NUMBER OF SEQUENCES: 23
CORRESPONDENCES.
ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: SOFTWARE BACKER RELEASE #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/615,271 FILING DATE: 20-JUN-1996 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49.8%; Score 607.5; DB 2; 55.6%; Pred. No. 1.1e-51; tive 36; Mismatches 49;
                                                                                                                                                                                                                                                                                                                                        CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 10, Application US/09074660
Patent No. 6020183
GENERAL INFORMATION:
APPLICANT: LOOSMORE, Sheena M.
APPLICANT: YANG, Yan-Ping
APPLICANT: CHONG, Pele
APPLICANT: OOMEN, Raymond P.
                                   Sequence 10, Application US/08615271
Patent No. 5981503
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 10:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (416) 595-1153
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 228 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SGGPLVCQKGNTWVLIGI 231
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amino acid
EDNESS: single
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Matches 110; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                  ADDRL.
STREET: 6t..
TTW: Toronto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-615-271-10
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APPLICANT: OOMEN, Raymond P.
APPLICANT: KLEIN, Michel H.
TITLE OF INVERTION: Analog of Haemophilus Hin47 Protein with
TITLE OF INVERTION: Analog of Haemophilus Hin47 Protein with
TITLE OF INVENTION: Reduced Protease Activity
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G IR7
COMPUTER: EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
CHIRLY DATA: DATA: DATA:
CHIRLY DATA: DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/487,167
FILING DATE: 07.JUN-1995
FILING DATE: 07.JUN-1995
FILING DATE: 26.AGG-1994
FILING DATE: 26.AGG-1994
FILING DATE: 21.JUL-1994
APPLICATION NUMBER: US 08/278,091
FILING DATE: 21.JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I.
FREISTRATION NUMBER: 24,973
REGISTRATION NUMBER: 24,973
REFRENCE/DOCKET NUMBER: 1038-730 MIS:jb
FILEPHONE: (416) 595-1163
FILEPHONE: (416) 595-1163
FILEPHONE: A163
FILE
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Search completed: December 20, 2002, 15:20:36 Job time : 14.087 secs

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Q9er05 mus musculu Q9d7p8 mus musculu Q9d960 mus musculu Q9ed22 ratus morv Q9w7q4 paralichthy Q9w7q3 paralichthy Q9c36 mus musculu Q9c35 mus musculu Q9d8x8 mus musculu
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OgG628 mus musculu
OgG719 mus musculu
OgC977 gadus morhu
Og577 gadus morhu
Og58w7 bos taurus
O9w7q1 paralichthy
                                                                   December 20, 2002, 15:14:08; Search time 28.6087 Seconds (without alignments) 1663.721 Million cell updates/sec
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                                                                                                                   US-09-856-319B-4_COPY_34_264
1252
1 IUNGENAVPGSWFWQVSLQD......AMYTRVSKFSTWINQVMAYN 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Description
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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                                                                                                                                                                                                        671580 seqs, 206047115 residues
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                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                              OM protein - protein search, using sw model
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092077
095KW7
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Q9D7P8
Q9D7P8
Q9W7Q4
Q9W7Q3
Q9C86
Q9CR35
Q9DR35
Q9DR35
Q9DR35
Q9DR35
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Gapop 10.0 , Gapext 0.5
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sp_human:*
sp_invertebrate:*
sp_mammal:*
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sp_unclassified:*
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sp_bacteriap:*
sp_archeap:*
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sp_bacteria:*
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Match Length DB
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1199
841.5
749.5
727.5
719.5
719.5
712.5
712.5
712.5
811.5
811.5
494.5
493
                                                                                                                      Title:
Perfect score:
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No.
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112
113
115
115
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ALIGNMENTS

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PROSITE; PS00135; TRYPSIN_SER; 1.
                                                                                  SEQUENCE
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              SWR
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STRAIN-C5DEL/GJ; TISSUE-TONGUE;

Kawai J., Shinadawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Rawai J., Shinadawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Rawai J., Shinadawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A rakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A Aizawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

A Saito T., Okazaki Y., Gojobori T., Bono H., Rasukawa T., Saito R.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Schrim L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

Sakai K., Okido T., Furuno M., Anon H., Baldarelli R., Barsh G.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Lyons P., Marchlonni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Nordone P., Ring B., Ringwald K., Wentz C., Whittaker C., Willming L.,

Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   154 TCVTTGWGRISGVGNVTPARLQQVVLPLVTVNQCRQYWGARITDAMICAGGSGASSCQGD 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 TCVTTGWGRISGVGNVTPARLQQVVLPLVTVNQCRQYWGARITDAMICAGGSGASSCQGD 180
                                                                                                                                                                                                                                                                                                                                                                   SNAEPVQVLSIARAITHPNWNANTMNNDLTLLKLASPARYTAQVSPVCLASTNEALPSGL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                   94 SNAEPVQVLSIARAITHPNWNANTMNNDLTLLKLASPARYTAQVSPVCLASTNEALPSGL 153
                                                                                                                                                                                                                                                              14 INTELLIBERAVPGSWPWQVSLQDNTGFHFCGGSLISPNWVVTAAACQVTPGRHFVVLGEYDRS 93
                                                                                                                                                         Gaps
                                                                                                                                                                                                                         1 IVNGENAVPGSWPWQVSLQDNTGFHFCGGSLISPNWVVTAAHCQVTPGRHFVVLGEYDRS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ·!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                             ;
                                                                       100.0%; Score 1252; DB 11; Length 264; llarity 100.0%; Pred. No. 9.7e-107; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 SGGPLVCQKGNTWVLIGIVSWGTKNCNIQAPAMYTRVSKFSTWINQVMAYN 231
1D979709A07056C2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                264
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PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00202; Tryp_SPC; 1.
PR0SITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
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InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
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       28135 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2002 (TrEMBLrel. 17,
01-JUN-2002 (TrEMBLrel. 21,
18100004D15R1k protein.
CTRL OR 1810004D15R1K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 409:685-690(2001)
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       264 AA;
                                                                                                                Local Similarity
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                                                                                                                                                  231;
       SEQUENCE
                                                                              Query Match
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                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                   61
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09D7P8
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Rawai J., Shinagawa A., Shipata K., Yoshino M., Itoh M., Ishli Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Arawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Ra Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kedlell E., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Wynshaw Boris A., Yoshida K., Hasegawa Y., Kawaii H., Kohtsuki S.,
RA Hayashizani Y., Storik K., Hasegawa Y., Kawaii H., Kohtsuki S.,
RA Hayashizani Y., Storik K., Hasegawa Y., Kawaii H., Kohtsuki S.,
                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                     61 SNAEPVQVLSIARAITHPNWNANTMNNDLTLLKLASPARYTAQVSPVCLASTNEALPSGL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 TCVTTGWGRISGVGNVTPARLQQVVLPLVTVNQCRQYWGARITDAMICAGGSGASSCQGD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94 SNAEPVQVLSIARAITHPNWNANTMNNDLTLLKLASPARTTAQVSPVCLASTNEALPSGL 153
                                                                                                                                                                                                                                                                           93
                                                                                                                                                       Gaps
                                                                                                                                                                                                              1 IVNGENAVPGSWPWQVSLQDNTGFHFCGGSLISPNWVVTAAHCQVTPGRHFVVLGEYDRS 60
                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                    ö
                                                                                      Length 264;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                            28167 MW; 1D979469A07056C2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                      Score 1248; DB 11;
Pred. No. 2.3e-106;
                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00089; trypsin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=C57BL/6J; TISSUE=PANCREAS;
MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00722; CHYMOTRYPSIN. SMART; SM00020; Tryp_SPc; 1.
                                                                                      99.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AK007333; BAB24967.1;
HSSP; P00766; 4CHA.
   protease.
                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 409:685-690(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1810004D15Rik protein.
CTRL OR 1810004D15RIK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEROPS; S01.256; -.
MGD; MGI:88558; Ctrl.
                                                                                      Query Match
Best Local Similarity
                            264 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRYPSIN FAMILY
Hydrolase; Serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                Matches 230;
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Matches 153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                           09W7Q4
09W7Q4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180
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                                                                                                                     RESULT 5
Q9W7Q4
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                                                                                                                                                                                                                                                                                                                                                 095028.
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 21, Last annotation update)
Chymopasin.
Rattus norvegicus (Rat).
Bukaryota; Metazoa (Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutherla; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                61 SNAEPVQVLSIARAITHPNWNANTMNNDLTLLKLASPARYTAQVSPVCLASTNEALPSGL 120
                                                                                                                                                                             TCVTTGWGRISGVGNVTPARLQQVVLPLVTVNQCRQYWGARITDAMICAGGSGASSCQGD 180
                                                                                                                                                                                                                        SNAEPVQVLSIARAITHPNWNANTMNNDLTLLKLASPARYTAQVSPVCLASTNEALPSGL 120
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                                                                                                Gaps
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                                                                                                                     1 IVNGENAVPGSWPWQVSLQDNTGFHFCGGSLISPNWVVTAAHCQVTPGRHFVVLGEYDRS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BJ databases.
S1; ALSO KNOWN AS
                                                                        DB 11; Length 264;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 264;
                                                                                                                                                                                                                                                           SGGPLVCQKGNTWVLIGIVSWGTKNCNIQAPAMYTRVSKFSTWINQVMAYN 231
                                                                                                                                                                                                                                                                      214 SGGPLVCQKGNTWVLIGIVSWGTKNCNIQAPAMYTRVSKFSTWINQVMAYN 264
                                                                      Score 1242; DB 11; Length
Pred. No. 8e-106;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00089; trypsin; 1.

PRINTS, PR00722; CHYMOTRYPSIN.

SMART; SM00020; Tryp_SPC; 1.

PROSITE; PS00134; TRYPSIN_DOM; 1.

PROSITE; PS00135; TRYPSIN_LIS; UNKNOWN_1.

PROSITE; PS00135; TRYPSIN_LSR; 1.

Hydrolase; Serine profease.

SEQUENCE 264 AA; 28116 MW; F9ED5D210FD3500E CRC64;
                                                   28151 MW; 1D979719E07C16DE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95.8%; Score 1199; DB 11; 92.6%; Pred. No. 6.9e-102; iive 16; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Molecular cloning of rat chymopasin.";
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ of SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI EMBL; AB020157; BAB20287.1; -. HSSP; P00766; 4CHA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-RAT PANCREAS;
Sogame Y., Mitsui S., Kataoka K., Kashima K.,
Yamaguchi N.;
                                                                                                                                                                                                                                                                                                                                           264 AA
TRYPSIN_DOM; 1.
TRYPSIN_HIS; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001314; ChymotrypsIn.
InterPro; IPR001254; Ser_protease_Try.
                                                                                                                                                                                                                                                                                                                                           PRT;
  PROSITE; PS50240; TRYPSIN_DOM; 1. PROSITE; PS00134; TRYPSIN_HIS; UNK PROSITE; PS00135; TRYPSIN_SER; 1. Hydrolase; Serine protease. Secure 264 AA; 28151 MW; 1DS
                                                                       99.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                              Matches 230; Conservative
                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEROPS; S01.256;
                                                                        Query Match
                                                                                    Local
                                                                                                                                                                                                                                                                                                                                          09E0Z8
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Matches
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TCVTTGWGRISGVGNVTPARLQQVVLPLVTVNQCRQYWGARITDAMICAGGSGASSCQGD 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 SNAEPVQVLSIARAITHPNWNANTMNNDLTLLKLASPARYTAQVSPVCLASTNEALPSGL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32 IVNGETAVSGSWPWQVSLQDGRGFHFCGGSLISPYWVVTAAHCTVSPRNHRVILGEHDRQ 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Paralichthys Olivaceus (Flounder).
Eukaryota: Metazoa: Chordata: Cranlata: Vertebrata; Euteleostoml;
Actinopterygli: Teleostel; Euteleostel; Neoteleostel;
Acanthomorpha: Acanthopterygli: Percomorpha: Pleuronectlformes;
Pleuronectoldel: Paralichthyidae; Paralichthys.
                               TISSUE-PANCREAS;
Suzuki T., Srivastava A.S., Kurokawa T.;
Japanese flounder mRNA for chymotrypsinogen l.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
FRYPSIN FAMILY.
HSSP; P00763; BAA82365.1; --
HSSP; P00763; IDPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 IVNGENAVPGSWPWQVSLQDNTGFHFCGGSLISPNWVVTAAHCQVTPGRHFVVLGEYDRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       152 KCVTTGWGRTGQTS--SPRYLQQTSLPLLSPAQCKQYWGYNRITDAMICAGASGVSSCQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <u>ښ</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 13; Length 261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DSGGPLVCQKGNTWVLIGIVSWGTKNCNIQAPAMYTRVSKFSTWINQVMAYN 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28184 MW; D7090A9D65395B7D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1999 (TrEMBLrel. 12, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67.2%; Score 841.5; DB 1
65.9%; Pred. No. 3.7e-69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPRO01314; Chymotrypsin.
InterPro; IPR00124; Ser_protease_Try.
InterPro; IPR00124; Ser_protease_Try.
PRINTS; PR00089; trypsin; I
PRINTS; SW00032; CHYMOTRYPSIN.
SWART; SW00030; TRYP_SRC; II.
PROSITE; PS500134; TRYPSIN_DM;
PROSITE; PS00134; TRYPSIN_ER; I.
PROSITE; PS00134; TRYPSIN_ER; I.
PROSITE; PS00135; TRYPSIN_ER; I.
PROSITE; PS00135; TRYPSIN_SER; I.
PROFICE: 261 AA; 28184 WW; D7090A9D65395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                        01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel. 12, (TrEMBLrel. 12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Chymotrypsinogen 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=8255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEROPS; S01.256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9W7Q3
ID Q9W7Q3
AC Q9W7Q3;
DT 01-NOV-1999 ('
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 SNAEPVQVLSIARAITHPNWNANTMNNDLTLLKLASPARYTAQVSPVCLASTNEALPSGL 120
                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83
                                                                                                                                                                                                                                                                                                                                                                                                                                           1 IVNGENAVPGSWPWQVSLQDNTGFHFCGGSLISPNWVVTAAHCQVTPGRHFVVLGEYDRS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TSEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE-21085660; Pubmed-11217851;

Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

Arakawa T., Izawa M., Nishi K., Kiyosawa H., Rondo S., Yamanaka I.,

Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
                       Paralichthys olivaceus (Flounder).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygli; Neopterygli; Teleostel; Butleostel; Neoteleostel;
Acanthomorpha; Acanthopterygli; Percomorpha; Pleuronectiformes;
Pleuronectoidei; Paralichthyidae; Paralichthys.
                                                                                                                                          Suzuki T., Srivastava A.S., Kurokawa T.;
"Japanese flounder mRNA for chymotrpsinogen 2.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPEIN FAMILY.
EMBL; AB029754; BAA82366.1; -.
HSSP; P00766; 1CHG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          150 KCVTSGWGLTRHNAPDTPALLQQAALPLLINDDCRRYWGNKISNLMICAGASGASSCMGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                   ij
                                                                                                                                                                                                                                                                                                                                                                                       59.9%; Score 749.5; DB 13; Length 260; 57.6%; Pred. No. 9.8e-61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  210 SGGPLVCQKAGAWTLVGIVSWGSGTCTPIMPGVYARVTELRAWMDQTIANN 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 SGGPLVCQKGNTWVLIGIVSWGTKNCNIQAPAMYTRVSKFSTWINQVMAYN 231
                                                                                                                                                                                                                               MEROPS; S01.152; ...
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001354; Ser_protease_Try.
Pfam; PP00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM0020; Tryp_SPC, 1.
PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
PROSITE; PS00135; TRYPSIN_ESR; 1.
PHOTOJASE; Scine protease.
SEQUENCE 260 AA; 27793 MW; 9F583044E22F78C0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                    62; Indels
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                  35;
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                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 133; Conservative
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                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
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                                                                                                                             TISSUE=PANCREAS;
                                                                                        NCBI_TaxID=8255
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Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schrilla L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Frurno M., Anno H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujite M., Gariboldi M., Gustincio S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchioni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sazaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Manshalboit S., Marchelli R., Kohtsuki S.,
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MEDLINE=21085660; PubMed=11217851;
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                 Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection.";
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 58.1%; Score 727.5; DB 11; Best Local Similarity 56.3%; Pred. No. 1e-58; Matches 130; Conservative 37; Mismatches 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS, PRO072; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
PROSITE; PS00135; TRYPSIN_SER; 1.
Hydrolase; Serine protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MGD; MGI:1913723; 2200008D09R1K.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_fry.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRYPSIN FAMILY.
EMBL; AK003060; BAB22539.1;
HSSP; P00766; 1GCT.
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01-JUN-2002 (TrEMBLrel.
2200008D09Rik protein.
2200008D09RIK.
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Hayashizaki Y.;
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A Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
A Fleischmann W., Gaasterland T., Gissi C., King B., Rochiwa H.,
A Kuehl P., Lewis S., Marsuo Y., Nikaido I., Pesole G., Quackenbush J.,
Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
A Sakal K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
B Isake J., Boffelli D., Bolunga N., Carninci P., de Bonaldo M.F.,
A Blake J., Boffelli D., Bolunga N., Carninci P., de Bonaldo M.F.,
Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
A Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Suzuki H., Toyo-oka K., Wang K.H., Weltz C., Whittaker C., Wilming L.,
Mynshaw-Bonis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                            'Functional annotation of a full-length mouse cDNA collection.";
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-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS 7 SEMELARITY: BELONGS TO PEPTIDASE FAMILY: 1, ALSO KNOWN AS 7 SEMEL; AKO03079; BAB25971.1; -. EMBL; AKO03079; BAB25241.1; -. EMBL; AKO07815; BAB25241.1; -. EMBL; AKO07815; BAB25240.1; -. EMBL; AKO08815; BAB25280.1; -. EMBL; AKO0888; BAB25861.1; -. EMBL; AKO0888; BAB25861.1; -. EMBL; AKO0888; BAB25861.1; -. EMBL; AKO0888; BAB25861.1; -. EMBL; AKO0888; BAB25954.1; -. EMBL; AKO0889; BAB25954.1; -. EMBL; AKO0889; BAB25954.1; -. 
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Last annotation update)
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Best Local Similarity 56.3%; Pred. No. 1.6e-58;
Matches 130; Conservative 36; Mismatches 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM0020; Tryp_SPc; 1.
PROSITE; PS50240, TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
Hydrolase; Serine protease.
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MGD; MGI:1913723; 2200008D09Rik.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
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                                                                                                                                                                                                                                                                                                                         Hayashizaki Y.
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STRAINCSTBL/63; TISSUB-PANCREAS;

KATAINCSTBL/63; TISSUB-PANCREAS;

KATAINCSTBL/63; TISSUB-PANCREAS;

KATAINCSTBL/64; TISSUB-PANCREAS;

RATAWA J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Arawa T., Hara A., Fukuhishi Y., Konoo H., Adachi J., Fukuda S.,

A Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Rato T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

Radota K., Matsuda H.A., Ashburner M., Bataloy S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Bataloy S., Casavant T.,

Ruchin P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Sakai K., Okido T., Fruno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Ruconstein M.J., Bult C., Fletcher C., Fullita M., Gariboldi M.,

Ryons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodfiguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Saya T., Shibata Y., Storch K.-F.,

Wanshaw-Booris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Wanshaw-Booris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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Nature 409:685-690(2001).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
EMBL; AR007566; BAB25112.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 IVNGENAVPGSWPWQVSLQDNTGFHFCGGSLISPNWVVTAAHCQVTPGRHFVVLGEYDRS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C0638FB8F905A92F CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Chymotrypsin B precursor (EC 3.4.21.1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Score 719.5; DB 1
; Pred. No. 5.5e-58;
36; Mismatches 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PRO0722; CHYMOTRYPSIN.
SMORD20; TRYP_SPS: 1.
PROSITE; PS50240; TRYPSIN_DOW; 1.
PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_I.
PROSITE; PS00135; TRYPSIN_HIS; UNKNOWN_I.
Hydrolaes; Serine protease.
SEQUENCE 263 AA; 27898 MW; CO638FB8F9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEROPS; SOL.152; -. MGD: MGI-1913723; 2200008DD9R1K. InterPro: IPR001314; Chymotrypsin. InterPro: IPR001254; Ser_protease_Try.
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Matches 129; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00089; trypsin; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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SEQUENCE
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MEDLINE-21085660; PubMed=11217851;
MEDLINE-21085660; PubMed=11217851;
MEDLINE-21085660; PubMed=11217851;
Arakawa T., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arakawa T., Hara A., Fukunishi Y., Konoo H., Adachi J., Fukuda S.,
Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Saito F., Okazaki Y., Golobori T., Bonoo H., Rasukawa T., Saito R.,
Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 -SNAEPVQVLSIARAITHPNWNANTMNNDLTLLKLASPARYTAQVSPVCLASTNEALPSG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120 LTCVTTGWG--RISGVGNVTPARLQQVVLPLVTVNQCRQYWGAR-ITDAMICAGGSGASS 176
                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                     32 IVNGEEAVPHSWPWQVSLQQSNGFHFCGGSLINENWVVTAAHCNVRT-YHRVIVGEHDKS 90
                                                                                                                                                                                                                                                                                                                                                                                                                                      1 IVNGENAVPGSWPWQVSLQDNTGFHFCGGSLISPNWVVTAAHCQVTPGRHFVVLGEYDRS 60
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Gadus.
                                                                                            Spilliaert R., Gudmundsdottir A.; "Molecular Cloning of the Atlantic Cod Chymotrypsinogen B."; Microb. Comp. Genomics 5:41-50(2000).
-:- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 209 CMGDSGGPLVCQKDNVWTLVGIVSWGSSRCSVTTPAVYARVTELRGWVDQILAAN 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CQGDSGGPLVCQKGNTWVLIGIVSWGTKNCNIQAPAMYTRVSKFSTWINQVMAYN 231
                                                                                                                                                                                                                                                                                                                                                                               56.9%; Score 712.5; DB 13; Length 263; 54.9%; Pred. No. 2.4e-57; ive 41; Mismatches 58; Indels 7;
                                                                                                                                                                                                                                                                                                                                                        EF61B18A34EE5E7C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                              MEKUCE; SULLIAL,
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001354; Ser_protease_Try.
Pfam; PF00089; trypsin; 1.
PRINT; SW00020; Tryp.SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HS; UNKNOWN_1.
PROSITE; PS00135; TRYPSIN_ERS; 1.
PROSITE; PS00135; TRYPSIN_ERS; 1.
PGCSITE; PS00135; TRYPSIN_ERS; 1.
                                                                                                                                                                                                                                                                                                                                           CHYMOTRYPSIN B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               164 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
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                                                  SEQUENCE FROM N.A.
TISSUE-PYLORIC CAECA;
MEDLINE-20464334; PubMed-11011764;
                                                                                                                                                                                                                                                                                                                                                        263 AA; 28175 MW;
                                                                                                                                                            EMBL; AJ242521; CAB43766.1;
HSSP; P00766; 1CHG.
MEROPS; S01.152; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel. 17, (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 54.9
Matches 129; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0910001G08Rik protein.
CTRL OR 0910001G08RIK.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                          263
                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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                          NCBI_TaxID-8049;
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01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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STRAIN-CS5BL/6J; TISSUE-STOWACH;

KAWAI J., Shingaqwa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

KAWAI J., Shingaqwa A., Shibata K., Konno H., Adachi J., Fukuda S.,

Arakwawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

A Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Ruchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Schriml L.M., Stabuli F., Suzuki R., Tomita M., Wagner L., Washio T.,

Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Lyons P., Marchionni L., Mashina J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida R., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77 HPNWNA-NTMNNDLFLLKLASP-ARYTAQVSPVCLASTNEALPSGLFCVTTGWGRISGVG 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NVTPARLQQVVLPLVTVNQCRQYWGARITDAMICAGGSGASSCQGDSGGPLVCQKGNTWV 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                     "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53.8%; Score 674; DB 11; 82.2%; Pred. No. 4.5e-54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 4.5e-54;
5; Mismatches 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEROPS; S01.997; -.
MGD; MGI:88558; Ctrl.
InterPro; IPR001254; Ser_protease_Try.
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SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 409:685-690(2001).
EMBL; AK003074; BAB22549.1; -.
HSSP; P00763; 1DPO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hydrolase; Serine protease.
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Matches 129; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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01-JUN-2002 (TrEMBLrel.
2310074F01Rik protein.
ELA3B OR 2310074F01RIK.
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SEQUENCE FROM N.A.
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Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  114 EALPSGLTCVTTGWGRISGVGNVTPARLQQVVLPLVTVNQCRQ - YWGARITDAMICAGG 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | ||:| | :||||:| | :||||| | ELLPNGAPCYISGWGRLSTNGPL-PDKLQQALLPVVDYEHCSRWNWWGLSVKTIMVCAGG 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SGASSCQGDSGFLVCQKGN-TWVLIGIVSW-GTKNCN-IQAPAMYTRVSKFSTWINQVM 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DIQSGCNGDSGGPLNCPADNGTWQVHGVTSFVSSLGCNTLRKPTVFTRVSAFIDWIEETI 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-C57BL/63; TISSUE-TONGUE;
MEDLINE-21085660; PubMed-11217851;
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Flelschmann W., Gasterland T., Gissi C., King B., Kochiwa H.,
Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
                                                                                                                                                                                                                                                                                                                                                                                                               DRSSNAEPVQVLSI--ARAITHPNWNANTMN--NDLTLLKLASPARYTAQVSPVCLASTN 113
                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                          28 VVNGEEAVPHSWPWQVSLQYEKDGSFHHTCGGSLITPDWVLTAGHCISTSRTYQVVLGEH 87
                                                                                                                                                                                                                                                                                                                                                            57
                                                                                                                                                                                                                                                                                                                                                            1 IVNGENAVPGSWPWQVSLQ---DNTGFHFCGGSLISPNWVVTAAHCQVTPGRHFVVLGEY
                                                "Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                        DB 11; Length 269;
                                                                                                                                                                                                                                                                                           40.9%; Score 511.5; DB 11; Lengtn
44.0%; Pred. No. 6.3e-39;
Linatrhes 86; Indels
                                                                                                                                                                                                                                                                              28977 MW; 9F43F769DDB2A7CF CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      269 AA
                                                                                                                                       MGD; MGI:1915118, Ela3b.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
PRM01254; Ser_protease_Try.
PRMNTS; PR00722; CHYMOTRYPSIN.
SMART; SM0020; Tryp_SPC; 1.
PROSITE; PS50240; TRYESIN_DOM; 1.
PROSITE; PS00135; TRYESIN_LSER; 1.
Hydrolase; Serine protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
                                                                                                   EMBL; AK008858; BAB25932.1; -. HSSP; P05805; 1FON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2001 (TrEMBLrel. 17, Cr
01-JUN-2001 (TrEMBLrel. 17, La
01-JUN-2002 (TrEMBLrel. 21, La
2310074F01Rik protein.
ELA3B OR 2310074F01RIK.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                   Best Local Similarity 44.0
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                              269 AA;
                                                                                      TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID-10090;
                                     Hayashizaki Y.;
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                                                                                                                                                                                                                                                                              SEQUENCE
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Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
A bronstein M.J., Bult C., Fletcher C., Fujita M., Garboldi M.,
A Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N. H.,
Iyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
A Nordone P., Ring B., Ringwald M., Rodiiguez I., Sakamoto N.,
A Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
A Sazuki H., Toyo-oka K., Wang K.H., Weltz C., Whittaker C., Wilming L.,
A Wanshaw Booris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
A Hayashizaki Y.,
Bructional annotation of a full-length mouse cDNA collection.";
C "I SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI; ALSO KNOWN AS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SGASSCOGDSGGPLVCQKGN-TWVLIGIVSW-GTKNCN-IQAPAMYTRVSKFSTWINQVM 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EALPSGLTCVTTGWGRISGVGNVTPARLQQVVLPLVTVNQCRQ--YWGARITDAMICAGG. 171
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
Eukaryota; Neopterygii; Teleoste1; Euteleoste1; Neoteleoste1;
Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Gadus.
NCBL_TaxID-8049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-UNW-2002 (TrEMBLrel. 21, Last annotation update)
Elastase precursor (EC 3.4.21.37) (Leukocyte elastase) (Lysosomal elastase) (Neutrophil elastase) (Bone marrow serine protease)
(MEDULLASIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 IVNGENAVPGSWPWQVSLQ---DNTGFHFCGGSLISPNWVVTAAHCQVTPGRHFVVLGEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40.9%; Score 511.5; DB 11; Length 269; 44.0%; Pred. No. 6.3e-39; ive 37; Mismatches 86; Indels 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PERMIT PRO0089; trypsin; 1.
PRINTS; PR00722; CHYMORRYPSIN.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS00240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_LHIS; UNKNOWN_1.
HYGROLASE; SERINE PROFERSER; 1.
Hydrolase; Serine profease; Serine profease; SEQUENCE 269 AA; 28904 MW; C543F76957B2A7CE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_fry.
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269 AA; '29010 MW; 352E4202B04BBB2D CRC64;

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Hydrolase; Serine protease.
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SEQUENCE
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                Gudmundsdottir E., Spilliaert R., Yang Q., Craik C.S., Bjarnason J.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58 D-RSSNAEPVQVLSIARAITHPNWNANTMNNDLTLLKLASPARYTAQVSPVCLASTNEAL 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117 PSGLTCVTTGWGRISGVGNVTPARLQQVVLPLVTVNQCRQY--WGARITDAMICAGGSGA 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28 VVGGEDVRVHSWPWQASLQYKSGNSFYHTCGGTLIAPQWVMTAAHC-IGSRTYRVLGKH 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 IVNGENAVPGSWPWQVSLQDNTG---FHFCGGSLISPNWVVTAAHCQVTPGRHFVVLGEY 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seddi R., Guo X.-J., Chaix J.-C., Puigserver A.;
"Nucleotide sequence of a bovine pancreatic proproteinase E cDNA.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 175 -SSCQGDSGGPLVCQKGN-TWVLIGIVSWGTK-NCNI-QAPAMYTRVSKFSTWINQVM 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     206 LASCNGDSGGPLNCQNADGSWDVHGVVSFGSSMGCNYPKKPSVFTRVSAYIPWINNVW 263
                                                            encoding two distinct psychrophilic elastases.";
Comp. Biochem. Physiol. 113B:795-801(1996).
-!- CATALYTIC ACTIVITY: HYDROLYSIS OF PROTEINS, INCLUDING ELASTIN. PREFERENTIAL CLEAVAGE: VAL-I-XAA > ALA-I-XAA.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
01-MAR-2002 (Fragment).
Bos taurus (Boyine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Peccra; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77; Indels 12;
                               Gudmundsdottir A.; \mbox{"Isolation and characterization of two cDNAs from Atlantic cod <math display="inline">\mbox{"Isolation and characterization of two cDNAs from Atlantic cod }
                                                                                                                                                                                                                                                                                                                                                                   ACTIVATION PEPTIDE (POTENTIAL). ELASTASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 266;
                                                                                                                                                                                                                                                                                                                                                                                                       B786B52C71559E2E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 496; DB 13;
Pred. No. 1.6e-37;
                                                                                                                                                                                                       InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
Pfam: PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPC; 1.
PR0SITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_LIS; UNKNOWN_I.
PROSITE; PS00135; TRYPSIN_SER; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            269 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48; Mismatches
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InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00089; trypsin; 1.
PROSITE; PS00134; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                          POTENTIAL
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MEDLINE=96262679; PubMed=8925447;
                                                                                                                                                                                                                                                                                                                                                                                                       28533 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 101; Conservative
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Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                      266 AA;
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Best Local Similarity
                                                                                                                                            TRYPSIN FAMILY
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                                                                                                                                                                                              MEROPS; S01.155;
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                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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172 SGASSCQGDSGGPLVCQKGN-TWVLIGIVSW-GTKNCN-IQAPAMYTRVSKFSTWINQVM 228
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                                                                                                                                                                                                               58 DRS--SNAEPVQVLSIARAITHPNWNANTM--NNDLTLLKLASPARYTAQVSPVCLASTN 113
                                                                                                                                                                                                                                                                                                                 114 EALPSGLTCVTTGWGRISGVGNVTPARLQQVVLPLVTVNQCRQ--YWGARITDAMICAGG 171
                                                                                                                                     28 VVNGEDAVPYSWSWQVSLQYEKDGAFHHTCGGSLIAPDWVVTAGHCISTSRTYQVVLGEY 87
                                                         Gaps
                                                                                                       1 IVNGENAVPGSWPWQVSLQ---DNTGFHFCGGSLISPNWVVTAAHCQVTPGRHFVVLGEY 57
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148 DILPNEAPCYISGWGRLY-TGGPLPDFKLQEALLPVVDYEHCSQWDWWGITVKKTMVCAGG
                                                      13;
Length 269;
                                                      Indels
                                                   88;
  DB 6;
39.5%; Score 494.5; DB 6 43.2%; Pred. No. 2.3e-37;
                                                   37; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search completed: December 20, 2002, 15:18:57 Job time : 29.6087 secs
                                                   Matches 105; Conservative
                              Best Local Similarity
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     Query Match
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December 20, 2002, 15:12:13 ; Search time 35.6087 Seconds (without alignments) 864.421 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*/SIDS2/gcgdata/geneseqg-embl/AA1981.DAT:*/SIDS2/gcgdata/geneseqgp-embl/AA1981.DAT:*/SIDS2/gcgdata/geneseqgp-embl/AA1981.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1988.DAT:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  908470
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    908470 seqs, 133250620 residues
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Maximum Match 100%
Listing first 45 summaries
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1221
1 MLLLSLTLSLVLLGSSWGCG.....
                                                                                                                       OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		æ				
Result		Query				
No.	Score	Match	Match Length DB ID	DB	ID	Description
-	1221	100 0	:	21	AAR11710	CTORA Cataon control
•	1			1	OT LITTING	יותוומוז מבדדום לדסרם
7	1093	89.5		21	AAB11711	Mouse serine prote
e	966	81.6		21	AAB54077	Human pancreatic c
4	684.5			23	AAU82738	Amino acid sequenc
'n	657.5			21	AAY99596	Bovine chymotrypsi
9	621.5			22	AAB98504	Human chymotrypsin
7	472			7	AAP61724	Porcine elastase I
œ	472	38.7	269	æ	AAP70758	Pig pancreas elast
6	446.5			13	AAR29621	Porcine pancreatic
10	445			7	AAP60062	Sequence of himan

Human elastase II. Human pancreatic c Human pancreas ela Human protein SEQ Fusion gene with h Amino acid sequenc	00 0 00	Human PR0382 (UW03 Human PR0382 prote Human PR0 polypept Human membrane-typ Human trypsin fami Tumour associated Human TAGD-12, pro Human cancer assoc Human serine prote	yene y ovarla trypsi acid s aldecri inogen inogen
	A AP60058 8 AAP70759 23 AAU87691 21 AAB54243 AAP60059 22 ABG20513 7 AAP60061 7 AAP61076 23 ABB07285	21 AAB44250 22 AA41694 22 AA429055 22 AAE23020 23 AAE23020 21 AAB32246 22 AA068911 21 AA843572 23 AA843572	AAE1/9 ABP4194 AACE330 AACE3906 AACE29 AACE29 AACE29 AACE29
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### ALIGNMENTS

RESULT 1

/SIDS2/gcgdata/geneseg/genesegp-embl/AA1990.DAT:*/SIDS2/gcgdata/geneseg/genesegp-embl/AA1991.DAT:*/SIDS2/gcgdata/geneseg/genesegp-embl/AA1992.DAT:* /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT:* /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1994.DAT:* /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT:* /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1996.DAT:* /SIDS2/gcgdata/geneseq/geneseqp·embl/AA1997.DAT:*/SIDS2/gcgdata/geneseq/geneseqp·embl/AA1998.DAT:*/SIDS2/gcgdata/geneseq/geneseqp·embl/AA1999.DAT:* /SIDS2/gcgdata/geneseg/genesegp-emb1/AA2000.DAT:*/SIDS2/gcgdata/geneseg/genesegp-emb1/AA2001.DAT:* /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:

us-09-856-319b-2_copy_1_231.rag

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The invention relates to novel serine process's designated bases?

The invention also relates to vectors and transformants comprising BSSP5 nucleic acids; transgenic animals in which the expression level of BSSP5 can be varied; and an mBSSP5 knockout mouse. The invention additionally encompasses anti-BSSP5 knockout mouse. The invention additionally encompasses anti-BSSP5 antibodies and methods of production of such antibodies, methods of BSSP5 detection using the antibodies, and the antibodies, methods of BSSP5 detection using the antibodies, and the medical conditions, e.g., pancreatitis; A method for detecting pancreatitis comprising measuring BSSP5 concentration in the blood or urine, and a pancreatitis diagnostic agent containing an anti-BSSP5 untibody is also disclosed. Nucleocides encoding BSSP5 were initially isolated in a human brain conserved regions of serine proteases. The BSSP5 serine proteases and nucleocides encoding them are useful in detecting homologues, mutants and polymorphic variants in biological samples (e.g., blood, urine, brain, prostate gland, placenta, testis, pancreatitis and prostatic hypertrophy. Sequence AAB11710 represents murine BSSP5 (hBSSP5), and sequence AAB11711 represents murine BSSP5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGSLISQSWVVTAAHCNVSPGRHFVVLGEYDRSSNAEPLQVLSVSRAITHPSWNSTTMNN 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MLLLSLTLSLVLLGSSWGCGIPAIKPALSFSQRIVNGENAVLGSWPWQVSLQDSSGFHFC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        diagnostic marker; antibody; transgenic animal; Alzheimer's disease; epilepsy; cancer; inflammation; infertility; pancreatitis; prostatic hypertrophy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MLLLSLTLSLYLLGSSWGCGIPAIKPALSFSQRIVNGENAVLGSWPWQVSLQDSSGFHFC
polymorphic variants as markers for diagnosis of e.g. Alzheimer's disease, epilepsy, cancer and inflammation, using blood, urine, pancreas or other tissues
                                                                                                                          serine proteases designated BSSP5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 1221; DB 21; Length 264; 100.0%; Pred. No. 1.1e-98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BSSP5; serine protease; human; hBSSP5; mouse; mBSSP5; brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 LVTVNQCRQYWDSSITDSMICAGGAGASSCQGDSGGPLVCQKGNTWVLIGI 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse serine protease BSSP5 (mBSSP5) SEQ ID NO:4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                Claim 1; Page 51-52; 70pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB11711 standard; Protein; 264 AA
                                                                                                                          invention relates to novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 231; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       264 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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The invention relates to novel serine proteases designated BSSP5

(AABI1710-B11711), and to nucleic acids encoding them (AAA61733-A61734).

The invention also relates to vectors and transformants comprising BSSP5 nucleic acids; transgenic animals in which the expression level of BSSP5 can be varied; and an mBSSP5 knockout mouse. The invention additionally encompasses anti-BSSP5 antibodies and methods of production of such antibodies, methods of BSSP5 detection using the antibodies, and the use of BSSP5 proteins or fragments as diagnostic markers for certain medical conditions, e.g., pancreatitis. A method for detecting medical conditions, e.g., pancreatitis concentration in the blood or urine, and a pancreatitis diagnostic agent containing an anti-BSSP5 antibody is also disclosed. Nucleotides encoding BSSP5 were initially isolated in a human brain cDNA library using degenerate PCR primers (AAA61744-A61745) based on conserved regions of serine proteases. The BSSP5 serine proteases and nucleotides encoding than are useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     detecting homologues, mutants and polymorphic variants in biological samples (e.g., blood, urine, brain, prostate gland, placenta, testis, pancreas and spleen) as diagnostic markers for conditions such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alzheimer's disease, epilepsy, cancer, inflammation, infertility, pancreatitis and prostatic hypertrophy. Sequence AAB11710 represents human BSSP5 (hBSSP5), and sequence AAB11711 represents murine BSSP5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MLLLSLTLSLYLLGSSWGCGVPAITPALSYNQRIVNGENAVPGSWPWQVSLQDNTGFHFC
                                                                                                                                                                                                                      Serine proteases BSSP5, useful in detecting homologs, mutants and polymorphic variants as markers for diagnosis of e.g. Alzheimer's disease, epilepsy, cancer and inflammation, using blood, urine, pancreas or other tissues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 264;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 LVTVNQCRQYWGARITDAMICAGGSGASSCQGDSGGPLVCQKGNTWVLIGI 231
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                                                                                                                          Mitsui S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            89.5%; Score 1093; DB 21;
85.7%; Pred. No. 1.6e-87;
iive 21; Mismatches 12;
                                                                                                                          Yamaguchi N,
                                                                                                                                                                                                                                                                                                                             Claim 3; Page 55-56; 70pp; Japanese.
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                                                                                                                          Kominami K,
99WO-JP06473.
                                        98JP-0347806.
                                                                               (FUSO ) FUSO PHARM IND LTD
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N-PSDB; AAA61734.
                                                                                                                        Uemura H, Okui A,
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Best Local Similarity
Matches 198; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        264 AA;
19-NOV-1999;
                                      20-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-MAR-2001
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AAS AAC98773 to AAC99231 encode the human pancreatic cancer associated proteins, called pancreatic cancer antigens have cytostatic, cancer antigens have cytostatic, cancer antigens have cytostatic, cancer antigens have cytostatic, contraceptive, nootropic, immunomodulatory, relaxant, contraceptive, gynaecological, cardiant and antiinflammatory activities, and can be used in gene therapy. The polynucleotide and proteins can be used for preventing, treating, or ameliorating a medical condition or in assays for diagnosing a pathological condition or a susceptibility to one in a subject. Binding partners to the proteins and the activity of the proteins can be identified. The pancreatic cancer antigens can be used to detect, treat or prevent pancreatic disorders, especially cancer.

Agonists and antagonists to the antigens can be screened for. The pancreatic cancer antigen polynucleotides can be used to detect and hybridisation probes that can be used in chromosome mapping, linkage and alagnostic methods. The proteins can be used to densic and diagnostic methods. The proteins can be used to penerate antibodies which are used to purify, detect and target the polypeptides, including both in vivo and in vitro diagnostic and target the polypeptides, including the productive, gastrointestinal, pulmonary, cardiovascular, renal or reproductive, dastrointestinal, pulmonary, cardiovascular, renal or proteins can be used to prevent neural, immune system, muscular, ceproductive, dastrointestinal, pulmonary, cardiovascular, renal or proteins can be used to prevent neural, immune system, mesular, ceproductive, dastrointestinal, pulmonary, cardiovascular, renal or prevent expection of the present invention.
                   Human; pancreas; pancreatic cancer; pancreatic cancer antigen; detection; datacetis; ldentification; cytostatic; neuroprotective; mootropic; immunomodulatory; relaxant; contraceptive; gynaecological; antiinflammatory; cardiant; gene therapy; chromosome mapping; linkage analygsis; ilssue identification; itssue typing; forensic; neural; immune system; muscular; reproductive; gastrointestinal; pulmonary; cardiovascular; renal; proliferative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid that is a pancreatic cancer antigen for preventing, treating, or ameliorating a medical condition, particular pancreatic cancer, or for use in assays for diagnosing a pathological condition
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                      08-MAR-2000; 2000WO-US05989.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-579444/54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rosen CA, Ruben SM;
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                                                                                                                                                                                                                                                                               WO200055320-A1.
                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                          12-MAR-1999;
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Gaps 5 SLTLSLVLLGSSWGCGIPAIKPALSFSQRIVNGENAVLGSWPWQVSLQDSSGFHFCGGSL ö 81.6%; Score 996; DB 21; Length 192; 99.5%; pred. No. 3.3e-79; 1ve 0; Mismatches 1; Indels Query Match
Best Local Similarity 99.5
Matches 189; Conservative g ö

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Human, protease; cancer; immune-related disorder; cardiovascular disease; neuronal-associated disease; metabolic disorder; inflammatory disorder; nervous system disorder; sexual dysfunction; pain; mood disorder; hypertension; psychotic disorder; neurological disorder; disorder; neurological disorder; diso
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acids encoding novel human proteases, useful for useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sudarsanam S, Manning G, Caenepeel S;
                                                                                                                                                                                                                                                                                                                                                                                            Amino acid sequence of novel human protease #37.
                                                                                                                                                                                                            AAU82738 standard; Protein; 263 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ocular disease; cytostatic; enzyme.
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                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                  181 NQCRQYWGSS 190
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185 NQCRQYWDSS 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SUGE-) SUGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; ABK31780
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                23-APR-2002
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                                                                                                                                                                                                                                                                    AAU82738;
                                                                                                                                                   RESULT 4
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The present invention relates to the isolation of novel human proteases, and the nucleic acids encoding them. The sequences of the invention are useful for treating diseases and disorders such as cancers (e.g. breast, colon, lung), immune-related diseases and disorders (e.g. inflammatory diseases and asthma), cardiovascular diseases (e.g. restenosis and coronary thrombosis), brain or neuronal associated diseases, metabolic disorders (e.g. diabetes, obesity), inflammatory disorders (e.g. rheumatoid arthritis and psoriasis), central or peripheral nervous system diseases, migraines, pain, sexual dysfunction, mood disorders, attention disorders, cognition disorders, hypotension, hypertension, psychotic disorders, neurological disorders (e.g. Alzheimer's disease, parkinson's disease) and dyskinesias. infections caused by human immunodeficiency virus (HIV), and non-viral infections such as ocular disease (e.g. glaucoma) and macular degeneration. AAU82702-AAU82760 represent the novel human proteases of Length 263; DB 23; 56.1%; Score 684.5; 55.0%; Pred. No. 8e-5 Live 36; Mismatches Best Local Similarity 55.0 Matches 127; Conservative Similarity 263 AA; Sequence Query Match

Claim 6; Fig 2M; 313pp; English.

inflammatory disorders

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139 PVCLASSNEALTEGLTCVTTGWGRLSGVGNVTPAHLQQVALPLVTVNQCRQYWDSSITDS 198
                                                                                                                                                                                                            120 AVCLPSASDDFAAGTTCVTTGWGLTRYTNANTPDRLQQASLPLLSNTNCKKYWGTKIKDA 179
                                                                                              SPGRHFVVLGEYDRSSNAEPLQVLSVSRAITHPSWNSTTMNNDVTLLKLASPAQYTTRIS 138
                                          CGIPAIKPALSFSQRIVNGENAVLGSWPWQVSLQDSSGFHFCGGSLISQSWVVTAAHCNV
                                                                                                                                                                                                                                                                      180 MICAGASGVSSCMGDSGGPLVCKKNGAWTLVGI 212
                                                                                                                                                                                                                                                    MICAGGAGASSCOGDSGGPLVCQKGNTWVLIGI
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Best Local Similarity
Matches 113; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 O'Brien TJ,
                                                                                                                                                                                                                                                                                                                                                                                                                            AAB98504;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tumour
                    13
                                                                                              79
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                                                                                                                                                                                                                                                                                      a
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                                                                                                                                  임
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is bovine chymotrypsinogen. It was included in a review of sequence homologies of several plasminogen activators. Plasminogen is the principal serine protease zymogen in the extracellular fluids of vertebrates. Its active form, plasmin, is implicated in pericellular proteolysis associated with a wide range of physiological and pathological processes. Plasminogen expression is regulated by plasminogen activators which hydrolyse a peptide bond in plasminogen to spontaneously convert it to plasmin . The sequence homology analysis has identified a six amino acid peptide involved in plasminogen activation. This peptide is particularly useful when inserted between amino acid residues 644 and 645 of full length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  plasminogen. Novel plasminogen activators have been made based upon the plasminogen activation/recognition site of plasminogen binding proteins. The polypeptides are useful in preparing thrombolytic agents for treating blood clotting disorders such as heart attack.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polypeptide with plasminogen activator activity useful as thrombolytic agent for treating blood clot disorders e.g. heart attack, comprises 10 amino acid peptide fragment for recognition or activation of
                                                                                                                                    120 DITLLKLATPARFSQTVSAVCLPSADDDFPAGTLCATTGWGKTKYNANKTPDKLQQAALP 179
                                                          61 GGSLISEDWVVTAAHCGVRTS-DVVVAGEFDOGSDEENIOVLKIAKVFKNPKFSILTVNN 119
1 MASLWILSCFSLVGAAFGCGVPAIHPVLSGLSRIVNGEDAVPGSWPWQVSLQDKTGFHFC
                                      GGSLISQSWVVTAAHCNVSPGRHFVVLGEYDRSSNAEPLQVLSVSRAITHPSWNSTIMNN
                                                                                                                DVTLLKLASPAQYTTRISPVCLASSNEALTEGLTCVTTGWGRLSGVGNVTPAHLQQVALP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 245;
                                                                                                                                                                                                              LVTVNQCRQYWDSSITDSMICAGGAGASSCQGDSGGPLVCQKGNTWVLIGI 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bovine; plasminogen activator; cardiant; thrombolytic; heart attack; stroke; blood clotting disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53.8%; Score 657.5; DB 21;
ilarity 54.9%; Pred. No. 1.7e-49;
Conservative 37; Mismatches 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 35-36; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (OKLA-) OKLAHOMA MEDICAL RES FOUND.
                                                                                                                                                                                                                                                                                                                            AAY99596 standard; protein; 245 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99WO-US09991.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zhang XC, Tang JJN;
                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                            Bovine chymotrypsinogen A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-422975/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 117; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    245 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200032759-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                      13-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38-JUN-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           plasminogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30s taurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                AAY99596;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bovine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lin X,
                                                                                                              121
                                                                                                                                                                                          181
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                                                                                                                                                                                                                                                                                      RESULT 5
AAY99596
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ADG-15 is an extracellular serine protease. It was found that TADG-15 is over-expressed in ovarian tumours. TADG-15 protein or its fragments of 9-20 residues that lack TADG-15 protease activity are useful for a risk of getting an individual against TADG-15, having, suspected of having or at risk of getting cancer. Furthermore, the TADG-15 gene can be used as a diagnostic or therapeutic target in cancer. The present sequence was used in a sequence homology alignment with the catalytic domain of TADG-15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33 RIVNGENAVLGSWPWQVSLQDSSGFHFCGGSLISQSWVVTAAHCNVSPGRHFVVLGEYDR 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    termed tumor antigen-derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15 protein overexpressed in carcinomas and DNA encoding it, for diagnosis, treatment, prevention of cancer, particularly breast,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 22; Length 231;
                                                                                                                                                                                                                                                                         TADG-15; cytostatic; vaccine; ovarian tumour; cancer; antigen-derived gene 15; serine protease; chymotrypsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                            Human chymotrypsin serine protease catalytic domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50.9%; Score 621.5; DB 2
56.8%; Pred. No. 2.2e-46;
iive 31; Mismatches 54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 10; Fig 1; 130pp; English.
AAB98504 standard; Protein; 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0421213.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel extracellular serine
                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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30-APR-1993 (first entry)
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 RESULT 8
          AAP70758
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6
 152
                                             FCGGSLISQSWVVTAAHCNVSPGRHFVVLGEYDRSSNAEPLQVLSVSRAITHPSWNSTTM 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N -- NDVTLLKLASPAQYTTRISPVCLASSNEALTEGLTCVTTGWGRLSGVGNVTPAHLQQ 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : ||: ||||||| | :| || :| || skgndiallying skgndiallklaspyilidigiclpaagsilpnnyvcyvtgwgrlothg-aspdiloo 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The porcine elastase product may be efficiently expressed from a transformed host such as colibacillus or yeast, yielding the product more efficiently than spleen extraction. See also J61192288.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 LILSLTLSLVLLGSSWGCGIPAIKPALSFSQRIVNGENAVLGSWPWQVSLQ-DSSG--FH 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       177 VALPLVTVNQCRQ--YWDSSITDSMICAGAG-ASSCQGDSGGPLVCQKGN-TWVLIGI 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSNAEPLQVLSVSRAITHPSWNSTTMNNDVTLLKLASPAQYTTRISPVCLASSNEALTEG
          LTCVTTGWGRLSGVGNVTPAHLQQVALPLVTVNQCRQYWDSSITDSMICAGGAGASSCQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 269;
                                                                                                                                                                                                                                                                                                                                                       Biological prepn. of pig elastase {\rm II} - using DNA with base sequence coding for specified aminoacid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                             38.7%; Score 472; DB 7;
45.6%; Pred. No. 3e-33;
ilve 32; Mismatches 84
                                                                                                                                AAP61724 standard; Protein; 269 AA.
                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Fig 1; 11pp; Japanese
                                                                   DSGGPLVCQKGNTWVLIGI 231
||||||||||||
|DSGGPLVCQKDGAWTLVGI 198
                                                                                                                                                                                                                                                                                            85JP-0034050
                                                                                                                                                                                                                                                                           85JP-0034050
                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 45.6
Matches 109; Conservative
                                                                                                                                                                                                                                                                                                             (KIRI ) KIRIN BREWERY KK
                                                                                                                                                                                                                                                                                                                            WPI; 1986-262895/40.
N-PSDB; AAN60919.
                                                                                                                                                                                   Porcine elastase II.
                                                                                                                                                                                                   Colibacillus; yeast.
                                                                                                                                                                                                                                                                                                                                                                                                                                              269 AA;
                                                                                                                                                                                                                                       JP61192289-A
                                                                                                                                                                                                                                                                                            22-FEB-1985;
                                                                                                                                                                                                                                                                          22-FEB-1985;
                                                                                                                                                                  23-OCT-1991
                                                                                                                                                                                                                                                         26-AUG-1986
                                                                                                                                                                                                                        Sus scrofa.
                                                                                                                                                AAP61724;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                  153
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93
                                                                    213
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                                                                                                               RESULT 7
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N--NDVTLLKLASPAQYTTRISPVCLASSNEALTEGLTCVTTGWGRLSGVGNVTPAHLQQ 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence encoding pancreas elastase may be used to transform an expression system. The product is useful in rejuvenating the elasticity of the arterial wall, and improving unusual serum lipid levels and lipoprotein metabolism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 LLLSLTLSLVLLGSSWGCGIPAIKPALSFSQRIVNGENAVLGSWPWQVSLQ-DSSG--FH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              177 VALPLVTVNQCRQ--YWDSSITDSMICAGGAG-ASSCQGDSGGPLVCQKGN-TWVLIGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pancreas elastase prodn. used to improve lipoprotein metabolism comprises isolating RNA coding elastase, synthesising single and double chain cDNA and introducing recombinant into host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38.7%; Score 472; DB 8;
45.6%; Pred. No. 3e-33;
tive 32; Mismatches (
                                                                                                                                                                                                                                                                                   /note= "May be absent"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 480; 18pp; Japanese.
                                                                                                                                                                                                                                             Location/Qualifiers
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AAP70758 standard; Protein; 269
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                                                                                                                                                                 metabolism; lipid.
                                                                                                                                                                                                                                                                                                                                                                                                              85JP-0138494
                                                                                                                                                                                                                                                                                                                                                                                                                                                     85JP-0138494
                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best_Local Similarity *...
Matches 109; Conservative
                                                                                                                      Pig pancreas elastase-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1987-040875/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           269 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SANY ) SANKYO KK.
                                                                                                                                                                                                                                                                Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                            25-JUN-1985;
                                                                              9-APR-1991
                                                                                                                                                                                                                                                                                                                              JP62000276-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-JUN-1985;
                                                                                                                                                                 Lipoprotein
                                                                                                                                                                                                                                                                                                                                                                    06-JAN-1987
                                                                                                                                                                                                       Sus scrofa
                                        AAP70758;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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WPI; 1986-262894/40.
N-PSDB; AAN60706.
                                                                                                                                                                                                                269 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human elastase II.
                                                           SANY ) SANKYO
                                                                            Takiguchi Y,
Ohsumi J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JP61192288-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-FEB-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-FEB-1985;
       23-OCT-1985;
05-APR-1985;
                        27-APR-1985;
26-JUL-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-OCT-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-AUG-1986.
                                          02-DEC-1985;
                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAP61723;
                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                             132 QYTTRISPVCLASSNEALTEGLTCVTTGWGRLSGVGNVTPAHLQQVALPLVTVNQCRQ-- 189
                                                                                                                                                                                                                                                                                                                                                                                                                76 CNVSPGRHFVVLGEYDRSSNAEPLQVLSVSRA--ITHPSWNSTTMN--NDVTLLKLASPA 131
                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                          19 CGIPAIKPALSFSQRIVNGENAVLGSWPWQVSLQ-DSSGF--HFCGGSLISQSWVVTAAH 75
                        Pig; swine; bile acid; gall bladder; bile acid secretion promoters; liver function improvers; ss.
                                                                                                                                                                                                                                 This sequence represents porcine pancreatic elastase III. It was expressed in E. coli YA21 using the expression vector \mathtt{pELE001}. It may be used in bile acid secretion promoters and liver function
                                                                                                                                                                                                                                                                                                                 15;
                                                                                                                                                                                                                                                                                            36.6%; Score 446.5; DB 13; Length 253; 43.5%; Pred. No. 4.8e-31; Live 33; Mismatches 78; Indels 15;
                                                                                                                                                                                     Pig pancreas elastase protein - used in bile acid secretion promoters and liver function improvers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence of human pancreatic elastase IIA encoded on pH2E2
                                                                                                                                                                                                                                                                                                                                                                                                                                                    :| |:: :|:||| | | ||||||| : :| : |: WWGSTVKQTMVCAGGDIRSGCNGDSGGPLNCPAADGSWQVHGV 218
                                                                                                                                                                                                                                                                                                                                                                                                                                         190 YWDSSITDSMICAGGAGASSCQGDSGGPLVCQKGN-TWVLIGI 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Enzyme; serum lipoprotein metabolism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAP60062 standard; Protein; 269 AA
        Porcine pancreatic elastase III.
                                                                                                                                                                                                                Claim 1; Page 8; 10pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86EP-0302557,
                                                                                                       91JP-0092069
                                                                                                                         91JP-0092069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                               97; Conservative
                                                                                                                                           (SANY ) SANKYO CO LTD.
                                                    Sus scrofa domestica
                                                                                                                                                            WPI; 1992-428826/52.
                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                             253 AA;
                                                                                                                                                                      N-PSDB; AAQ31724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-APR-1986;
                                                                                                       23-APR-1991;
                                                                                                                         23-APR-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                     JP04325090-A
                                                                                      13-NOV-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EP198645-A.
                                                                                                                                                                                                                                                             improvers
                                                                                                                                                                                                                                                                             Sequence
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119 N--NDVTLLKLASPAQYTTRISPVCLASSNEALTEGLTCVTTGWGRLSGVGNVTPAHLQQ 176
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                                                                                                                                                                                                                                                                                                                                                                                                             The genetically engineered prod. can eliminate the dependency on human pancreas supplies for the elastase, and avoids antibody formation and possibility of anaphylaxis using porcine elastase.
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                                                                                                                                                                                                                                                                                                        - obtd.
                                                                                                                                                                        Τ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 36.4%; Score 445; DB 7; Length 269; Best Local Similarity 43.9%; Pred. No. 6.9e-31; Matches 105; Conservative 28; Mismatches 92; Indels
                                                                                                                                                                          Ohmine
                                                                                                                                                                                                                                                                                                      New genetically engineered human pancreatic elastase using hosts modified DNA coding for enzyme
                                                                                                                                                                          Eurukawa H,
                                                                                                                                                                          Kawashima I,
                                                                                                                                                                                                                                                                                                                                                                     Example; Page 14-15; 45pp; English.
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85JP-0236686.
85JP-0072308.
85JP-0091986.
85JP-0163964.
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                                                                                     85JP-0271128
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                                                                                                                                                                             Tani T,
                                                                                                                                                                                                                                       WPI; 1986-280300/43.
N-PSDB; AAN60076.
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JP62000276-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59 FCGGSLISQSWVVTAAHCNVSPGRHFVVLGEYDRSSNAEPLQVLSVSRAITHPSWNSTTM 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57 TCGGSLIANSWVLTAAHCISSSRTYRVGLGRHNLYVAESGSLAVSVSKIVVHKDWNSNQI 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid that is a pancreatic cancer antigen for preventing, treating, or ameliorating a medical condition, particular pancreatic cancer, or for use in assays for diagnosing a pathological condition
                                                                                                                                                                                                                                The human elastase product may be efficiently expressed from a transformed host such as collbacilius or yeast, yielding the product more efficiently than spleen extraction.

See also J61192289.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 LLLSLTLSLVLLGSSWGCGIPAIKPALSFSQRIVNGENAVLGSWPWQVSLQDSSG---FH 58
                                       Biologically producing human elastase ii - using DNA chain with biological prodn. capability for human elastase II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36.0%; Score 439.5; DB 7; Length 34.7%; Pred. No. 2.1e-30; tive 26; Mismatches 87; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        177 VALPLVTVNQCRQ--YWDSSITDSMICAGGAGA-SSCQGDSGGPLVCQ 221
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                                                                                                                                                                  Claim 1; Fig 1-2; 19pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 102; Conservative
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N-PSDB; AAC98889.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     269 AA;
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AAC98773 to AAC99231 encode the human pancreatic cancer associated proteins, called pancreatic cancer antigens, given in AAB54068 to AAB54466. The human pancreatic cancer antigens have cytostatic.

AAB54466. The human pancreatic cancer antigens have cytostatic, cancroprotective, nootropic, immunondulatory, relaxant, contraceptive, gynaecological, cardiant and antiinflammatory activities, and can be used for in gene therapy. The polynucleotide and proteins can be used for preventing, treating, or ameliorating a medical condition or in assays for diagnosing a pathological condition or a susceptibility to one in a subject. Binding partners to the proteins and the activity of the control of proteins can be identified. The pancreatic cancer antigens can be used to detect, treat or prevent pancreatic disorders, especially cancer.

Composition and antagonists to the antigens can be used to design nucleic catch hybridisation probes that can be used to design nucleic and hybridisation probes that can be used to design nucleic and diagnostic methods. The proteins can be used to generate antibodies which are used to purify, detect and target the polypeptides, including both in vivo and in vitro diagnostic and therapeutic methods. The proteins can be used to generate antibodies both in vivo and in vitro diagnostic and therapeutic methods. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 proteins can be used to treat or prevent neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal or proliferative disorders. AAC99232 to AAC99240 and AAB54467 represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 TCGGSLIANSWVLTAAHCISSSRTYRVGLGRHNLYVAESGSLAVSVSKIVVHKDWNSNQI 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 MIXTLLLSTLVAG-ALSCGDPTYPP---YVTRVVGGEEARPNSWPWQVSLQYSSNGKWYH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119 N--NDVTLLKLASPAQYTTRISPVCLASSNEALTEGLTCVTTGWGRLSGVGNVTPAHLQO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35.0%; Score 427.5; DB 21; Length 269; 43.9%; Pred. No. 2.3e-29; ive 26; Mismatches 89; Indels 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2..15
/note= "May be absent"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sest Local Similarity 43.9 Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             269 AA;
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13-APR-2000; 2000WO-US09973.
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         Tang YT,
Zhao QA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                              Sequence
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                             Xue AJ,
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Matches
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AAB36481
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
                                                                                                                                                                                                                                                                              FCGGSLISQSWVVTAAHCNVSPGRHFVVLGEYDRSSNAEPLQVLSVSRAITHPSWNSTTM 118
                                                                                                                                                                                                                                                                                                        119 N--NDVTLLKLASPAQYTTRISPVCLASSNEALTEGLICVTTGWGRLSGVGNVTPAHLQQ 176
                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                            LLLSLTLSLVLLGSSWGCGIPAIKPALSFSQRIVNGENAVLGSWPWQVSLQDSSG---FH 58
                                                                                                                                                                                                                                              1 MIRTLLLSTLVAG-ALSCGVSTYAPDMS---RMLGGEEARPNSWPWQVSLQYSSNGQWYH 56
                                                                                                                                                                                                                                                                                                                                               177 VALPLVTVNOCRQ--YWDSSITDSMICAGGAGA-SSCQGDSGGPLVCQKGN-TWVLIGI 231
                                                                                                                                                                                                                                                                                                                                                         Sequence encoding pancreas elastase may be used to transform an expression system. The product is useful in rejuvenating the elasticity of the arterial wall, and improving unusual serum lipid levels and lipoprotein metabolism.
                                                       Pancreas elastase prodn. used to improve lipoprotein metabolism -
comprises isolating RNA coding elastase, synthesising single and
double chain cDNA and introducing recombinant into host
                                                                                                                                                                                                         14;
                                                                                                                                                                                    ; Score 427; DB 8; Length 269;
; Pred. No. 2.6e-29;
36; Mismatches 91; Indels
                                                                                              Disclosure; Page 482; 18pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                  AAM78338 standard; Protein; 1052 AA
                                                                                                                                                                                     35.0%;
41.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human protein SEQ ID NO 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-0560875
2000US-0598075
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2000US-0663561
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2000US-0728422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                        98; Conservative
                           WPI; 1987-040875/06
                                                                                                                                                                                              Best Local Similarity
         (SANY ) SANKYO KK.
                                                                                                                                                                  269 AA;
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                                      N-PSDB; AAN71123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-FEB-2000;
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20-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-JUL-2000;
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15-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-AUG-2001.
                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                     AAM78338;
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   Ma Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          119 N--NDVTLLKLASPAQYTTRISPVCLASSNEALTEGLTCVTTGWGRLSGVGNVTPAHLQQ 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59 FCGGSLISQSWVVTAAHCNVSPGRHFVVLGEYDRSSNAEPLQVLSVSRAITHPSWNSTTM 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         117 SKGNDIALLKLANPVSLTDKIQLACLPPAGTILPNNYPCYVTGWGRLQTNG-ALPDDLKQ 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        177 VALPLVTVNQCRQ--YWDSSITDSMICAGGAGA-SSCQGDSGGPLVCQKGN-TWVLIGI 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fusion gene with human serine protease catalytic domain protein #12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Activation construct; catalytic; fusion gene; expression vector; proteolysis; serine protease; zymogen precursor; characterisation; analysis; modulator; identification.
                                                                                                                                                                                                                                        Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 LLLSLTLSLVLLGSSWGCGIPAIKPALSFSQRIVNGENAVLGSWPWQVSLQDSSG---FH
       Cao Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14;
       Xu C, Cao Y,
R, Wang ZW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1052;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
Drmanac RT, Asundi V, Zhou P,
Wang J, Zhang J, Ren F, Chen
Wejhrman T, Goodrich R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35.0%; Score 427; DB 22;
41.0%; Pred. No. 1.4e-28;
Live 36; Mismatches 91;
                                                                                                                                                                                                                                                                                                                                              Claim 20; Page 3226-3228; 6221pp; English.
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                                                                                                                                     WPI; 2001-476283/51.
N-PSDB; AAK51471.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
les 98; Conserv
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   Liu C, I
Wang D,
Yang Y, I
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The present invention describes an expression vector (I) comprising in frame and in order, a presequence, and a cloning site for the in frame insertion of catalytic domain cassette. (I) can be used as a modulator of proteins expressed from a zymogen activation construct. The recombinant catalytic domain of serine protease is useful for identifying compounds modulating the activity of proteases. Is expressed and activated from the zymogen activation construct. A method from the present invention comprises combining a modulator of the modulator on the protein of a protease and mesuring an effect of the modulator on the protein preferably inhibiting or enhancing its enzymatic activity or stimulation or inhibition of proteolysis mediated (by the expressed catalytic domain. The present sequence represents a fusion gene with a human serine protease catalytic domain protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ,,
                                                                                                                                                                      Expression vector for producing recombinantly producing serine protease domains, comprising a presequence, a prosequence, and a cloning site for the insertion of catalytic domain cassette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    166 VGNVTPAHLQQVALPLVTVNQCRQYWDSS-----ITDSMICAG--GAGASSCQGDSG 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52 QDSSGFHFCGGSLISQSWVVTAAHCNVSPGRHF-----VVLGEYDRSSNAEPLQVLSVSR 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    107 AITHPSWNSTTMNNDVTLLKLASPAQYTTRISPVCLASSNEALTEGLTCVTTGWGRLS-G 165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97; Indels 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 34.7%; Score 424; DB 21; Length 319; Best Local Similarity 35.9%; Pred. No. 5.8e-29; Matches 92; Conservative 39; Mismatches 97; Indels 28
                                                                                                                                                                                                                                                 Disclosure; Page 47-50; 89pp; English
                                                      (ORTH ) ORTHO-MCNEIL PHARM RES INC.
                                                                                             Darrow A, Qi J, Andrade-Gordon P;
                  99US-0303162.
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                                                                                                                                 WPI; 2000-687533/67.
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                  30-APR-1999;
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Search completed: December 20, 2002, 15:16:39 Job time : 37.6087 secs

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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.

- protein search, using sw model OM protein

December 20, 2002, 15:14:28; Search time 2.08696 Seconds Run on:

(without alignments)
1520.126 Million cell updates/sec

166 1 MLLLSLTLSLVLLGSSWGCGVPAITPALSYNQR 33 US-09-856-319B-4_COPY_1_33 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 segs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

S	Ţ	chymotrypsin-like	-	_	_	hypothetical prote	•—	monofunctional blo	pancreatic elastas	pancreatic elastas	hypothetical prote	probable sugar nuc	monofunctional bio	chitinase (EC 3.2.		peptide transport	potassium transpor	tyrosine protein k	e gluc	chymase (EC 3.4.21	EC 3	ol-cy	probable membrane	ÚS10 protein - hum	nitrite transport	endopeptidase Clp	cation-transportin	, hypothetical prote		
SUMMARIES		136	5	66	. ~	20	55	90	92	25	54	[]	31	90	91	8.	58	30	=	74	13	~	98	7	55	74	99	98	9(	
รเ	ΙD	13813	A21195	A31299	KYRTB	F90260	A49265	AE0906	S68826	S68825	T05664	B71511	AI0431	T10106	JE0346	T04378	T02268	T03180	AH0241	S23504	S26043	CBUTB	852098	QQBE07	T10255	A70204	F86709	A83108	A22706	
	DB	2	~	7	-	7	7	7	7	7	~	7	~	7	7	7	~	7	7	7	~	-	7	7	~	1	7	~	7	
	gth	264	263	263	263	835	231	242	268	268	466	219	241	292	557	579	826	1186	384	247	260	363	742	312	484	739	918	94	104	
ď	Query Match	90.4	45.8		40.4	33.4	33.1	33.1	33.1	33.1	33.1	31.3	31.3	31.3	31.3	31.3	30.7	30.7	30.4	30.1	30.1	30.1	30.1	29.8	29.8		29.8	29.5	29.2	
	Score	150	16	73	67	55.5		52	55	52	52	52	52	52	52	52	51	51	50.5	20	20	20	20	49.5	49.5	49.5		49	49	
	Result No.	7	7	m	4	S	9	7	60	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	

ATP synthase subun probable trypsin i	cal hydr	malx protein - Kle tricorn proteinase	chymotrypsin (EC 3 chymotrypsin (EC 3	chymotrypsin-like chymotrypsin (EC 3	chymotrypsin (EC 3 chymotrypsin (EC 3	probable DNA methy conserved hypothet	hypothetical prote
D86502 S16575	B69452 A70771	982383 B25025 D90495	C61414 B61414	A23473 KYBOB	KYBOA S47537	G83435 A83377	S38125
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141	319	310	16	126 245	245 263	304	418
29.5	29.5 29.5	29.5	28.9	28.9 28.9	28.9 28.9	28.9	28.9
4 4 9	4 4 4 0 0 0	48.5	4 4 8 8	4 4 8 8	4 4 8 8	<b>4</b> 4	48
30 31	33.2	30.0	37	39 40	41	44	45

#### ALIGNMENTS

C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Accession: 138136
E; Accession: 138136
Hum. Mol. Genet. 2, 1589-1595, 1993
A; Title: A tight cluster of five unrelated human genes on chromosome 16q22.1.
A; Reference number: 138136
A; Accession: 138136
A; Accession: 138136
A; MulD: 94093544; PMID: 8268911
A; Molecule type: DNA
A; Residues: 1-264 <RES> A;Cross-references: EMBL:X71874; NID:g406226; PIDN:CAA50710.1; PID:g406228 C;Genetics: chymotrypsin-like proteinase (EC 3.4.21.-) CTRL-1 - human

A;Gene: GDB:CTRL A;Cross-references: GDB:204061

A Map position: 16q22.1-16q22.1
A:Introns: 18/1; 52/3; 79/2; 106/3; 167/1; 211/3
C:Superfamily: trypsin; trypsin homology
C:Keywords: hydrolase; serine proteinase
F;34-257/Domain: trypsin homology <TRY>
F;75,121,214/Active site: H1s, Asp, Ser #status predicted

ö 90.4%; Score 150; DB 2; Length 264; 87.9%; Pred. No. 9.2e-12; ative 3; Mismatches 1; Indels Query Match Best Local Similarity 87.9% Matches 29; Conservative

ö

Gaps

1 MLLLSLTLSLVLLGSSWGCGVPAITPALSYNOR 33 ò Q

RESULT 2

Chymotrypsin (EC 3.4.21.1) 2 precursor - dog C;Species: Canis lupus familiaris (dog) C;Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 22-Jun-1999

C;Accession: A21195
R;Pinsky, S.D.; LaForge, K.S.; Luc, V.; Scheele, G.
Proc. Natl. Acad. Sci. U.S.A. 80, 7486-7490, 1983
A;Title: Identification of cDNA clones encoding secretory isoenzyme forms: sequence d A;Reference number: A21195; MUID:84170253; PMID:6584866
A;Accession: A21195

A;Status: preliminary

A; Molecule type: mRNA A; Residues: 1-263 <PIN>

A;Cross-references: GB:K01173; NID:q163945; PIDN:AAA30841.1; PID:q163946 S. Superfamally: trypsin, trypsin homology C;Keywords: hydrolase; protein digestion; serine proteinase F;34-256/Domain: trypsin homology <TRY>

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hypothetical protein SSO1079 [imported] - Sulfolobus solfataricus C;Species: Sulfolobus solfataricus C;Species: Sulfolobus Solfataricus C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001 C;Accession: F90260 R;She, Q: Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Ch Sine, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Ch Jofffies, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J. Submitted to GenBank, April 2001 A;Description: Sulfolobus solfataricus complete genome. A;Reference number: A99139 A;Accession: F902&60 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-835 < KUR> A;Residues: 1-835 < KUR> A;Residues: 1-835 < KUR> A;Cross-references: GB:AE006641; NID:g13814269; PIDN:AAK41341.1; GSPDB:GN00155 A;Genetics:
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A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: 1-197, 'L', 198-231 < RE2>
A; Cross-references: EMBL:U29875; NID:g1072039; PIDN:AAA90951.1; PID:g1072040
A; Cross-references: EMBL:U29875; NID:g1072039; PIDN:AAA90951.1; PID:g1072040
A; Coulpepper, J; Campbell, D; McClanahan, T; Zurawski, S; Bazan, J.F.; Felt, A.: Muench, M.: Relner, G.; Namikawa, R.; Rennick, D.; Roncarolo, M.G.; Zlotnik Nature 368, 643-648, 1994 L95428; PMID:g10551
A; Reference number: 543290; MUID:94195428; PMID:g145851
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 13-dan-1995 #sequence_revision 13-Jan-1995 #text_change 08-oct-1999
C;Accession: A49265; I49347; I49346; S43290
B;Lyman, S.D.; James, L.; Vanden Bos, T.; de Vries, P.; Brasel, K.; Gliniak, B.; Holl D:; Williams, D. B.; Beckmann, M.P.
Cell 75, 1157-1167, 1993
A;Title: Molecular cloning of a ligand for the flt3/flk-2 tyrosine kinase receptor: a A;Reference number: A49265; MUID:94084791; PMID:7505204
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A;Molecule type: DNA
A;Residues: 1-163,'G',165,'HYAG' <RES>
A;Cross-references: EMBL:U29875; NID:g1072039; PIDN:AAA90952.1; PID:g1072041
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A.Status: preliminary
A.Molecule type: mRNA
A.Status: L-IMA
A.Status: J-231 - J-IMA
A.Status: J-195
A.Status: J-196
A.Stat
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Pred. No. 28;
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                                       MLLLSLTLSLVLLGSSWGCGVPAITPALS
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A; Residues: 1-197, 'L', 198-231 <HAN>
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Best Local Similarity 44.8%;
Matches 13; Conservative
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A;Title: Molecular cloning and nucleotide sequence of human pancreatic prechymotrypsinog A;Reference number: A31299; MUID:89134264; PMID:2917002
A;Accession: A31299
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A;Title: Isolation and sequence of a rat chymotrypsin B gene. A;Reference number: A22658; MUID:85054881; PMID:6209274
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N;Alternate names: chymotrypsinogen B
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus horvegicus (Norway rat)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 18-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Homo sapiens (man)
C;Date: 08-Jun-1989 #sequence_revision 08-Jun-1989 #text_change 22-Jun-1999
C;Accession: A31299
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A; Residues: 1-263 <BEL>
A; Residues: 1-263 <BEL>
A; Cross-references: GB:K02298; NID:g203653; PIDN:AAA98732.1; PID:g203654
C; Genetics:
A; Introns: 18/1; 52/3; 79/2; 105/3; 166/1; 210/3
C; Superfamily: trypsin; trypsin; homology
C; Superfamily: trypsin; trypsin; protein digestion; serine proteinase
F; 1-18/Domain: signal sequence #status predicted <SIG>
F; 19-33/Domain: propeptide #status predicted <RG>
F; 19-33/Domain: propeptide #status predicted <AMT>
F; 34-256/Domain: trypsin homology <TRY>
F; 75,120,213/Active site: His, Asp, Ser #status predicted
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                                                                               DB 2; Length 263;
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                                                                           Score 76; DB 2; Length 263
Pred, No. 0.024;
3; Mismatches 10; Indels
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A.Map position: 16q23.1-16q23.1
C.Superfamily: trypsin; trypsin homology
C.Steywords: hydrolase; protein digestion; serine proteinase
F:34-256/Domain: trypsin homology CTRY>
F:75,120,213/Active site: His, Asp, Ser #status predicted
F;75,120,213/Active site: His, Asp, Ser #status predicted
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                                                                           Query Match 45.8%;
Best Local Similarity 55.2%;
Matches 16; Conservative
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Matches 13; Conserv
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A;Molecule type: mRNA
A;Residues: 1-263 <TOM>
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S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitche
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N;Alternate names: caldecrin isoform 1
C;Species: Homo sapiens (man)
C;Date: 04-Dec-1997 #sequence_revision 12-Dec-1997 #text_change 28-May-1999
C;Accession: S68825
R;Tomomura, A.; Akiyama, M.; Itoh, H.; Yoshino, I.; Tomomura, M.; Nishii, Y.; Noikuz
FBSS Lett. 386, 26-28, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Accession: T05664
R; Bevan, M.; Wedler, H.; Kutzner, M.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Mayer, submitted to the Protein Sequence Database, February 1999
A; Reference number: 215420
A; Accession: T05664
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C,Species: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 20-Apr-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein F22113.130 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: mRNA
A;Residues: 1-268 <TOM>
A;Cross-references: GB:S82198; NID:g1839466; PIDN:AAB47104.1; PID:g1839467
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C; Superfamily: trypsin; trypsin homology
C; Superfamily: trypsin; trypsin homology
C; Reywords: hydrolase; pancreas; serine proteinase; zymogen
E;11-16/Domain: signal sequence #status predicted <SIG>
F;17-29/Domain: propeptide #status predicted <PRO>
F;30-268/Product: pancreatic elastase isoform 1 #status predicted
F;30-262/Domain: trypsin homology <TRY>
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A;Experimental source: cultivar Columbia; BAC clone F22113
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31.0%; Pred. No. 19;
Live 10; Mismatches
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A;Introns: 50/3; 87/1; 148/3; 178/2; 265/3; 349/3
A;Note: F22113.130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 55;
Pred. No.
          LLSLTLSLVLLGSSWGCGVPAITPALS 29
                                                  1 HIGITVLAALLACASSCGVPSFPPNLS 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 LLSLTLSLVLLGSSWGCGVPAITPALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 31.09
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 40.79
Matches 11; Conservative
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Science 282, 754-759, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Residues: 1-466 <BEV>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Accession: B71511
R; Stephens, R.S.; Ka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: S68825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Genetics
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B71511
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          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 monofunctional biosynthetic peptidoglycan transglycosylase (EC 2.4.2.-) [imported] - Sal Riborational biosynthetic subsp. enterica serovar Typhi CiSpecies: Salmonella enterica subsp. enterica serovar Typhi ciborate: has also been called Salmonella typhi CiDate: Ob-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 27-Nov-2001 Ext. Conserton, D.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P. Nutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A; Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serova A; Accession: AsD0906 A; Status: Preliminary A; Molecule type: DNA A; Reference number: AB0502; PMID:11677608 A; Residues: 1-242 cPAR> A; Cross-references: GB:AL513382; PIDN:CAD07843.1; PID:g16504391; GSPDB:GN00176
                                           4-Val
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R.Tomomura, A.; Aliyama, M.; Itoh, H.; Yoshino, I.; Tomomura, M.; Nishii, Y.; Noikura, FEBS Lett. 386, 26-28, 1996
A.Title: Molecular cloning and expression of human caldecrin.
A.Reference number: S68825; MuID:96221265; PMID:8635596
A.Accession: S68826
A.Accession: S68826
A.Reference number: s68826
A.Reference number: Jege 2009
A.Residues: 1-268 < TOM>
A.Residues: 1-268 < TOM>
A.Residues: 1-268 < TOM>
A.Residues: Trypsin; 
                                       in having
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C;Date: 04-Dec-1997 #sequence_revision 12-Dec-1997 #text_change 30-Jan-1998
C;Accession: S68826
                                                                                                                                                                                                                                                                                     Gaps
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                                           2a
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A; Experimental source: clone T110
A; Note: the sequence from F19. 2c is inconsistent with that from F19.
C; Genetics: 11/3; 49/3; 67/3; 115/3; 164/1; 224/3
C; Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 55; DB 2; Length 268;
Pred. No. 12;
5; Mismatches 11; Indels
                                                                                                                                                                                                             Length 231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 242;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pancreatic elastase (EC 3.4.21.36) isoform 2 precursor - human N;Alternate names: caldecrin isoform 2
                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: mtgA
C;Keywords: glycosyltransferase; pentosyltransferase
                                                                                                                                                                                                                5
                                                                                                                                                                                                             Score 55; DB 2
Pred. No. 10;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 55; DB 2
Pred. No. 11;
3; Mismatches
                                                                                                                                                                                                                33.18;
61.18;
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Best Local Similarity 40.7%;
Matches 11; Conservative
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58.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                      192 LLLLLLPLTLVLLAAAWG 209
                                                                                                                                                                                                                                                                                                                                                      1 MLLLSLTLSLVLLGSSWG 18
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                                                                                                                                                                                                                Query Match 33.19
Best Local Similarity 61.19
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17 WGCGVPAITPALSYNOR 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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es 10; Conserv
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Matches
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Indels

Length 292;

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Score 52; DB 2 Pred. No. 30; 3; Mismatches

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F;44-292/Product: chitinase #status experimental <MAT>
F;48-284/Domain: plant chitinase homology <PCH>
                                                                                                                                                                                                  1 MLLLSLTLSLVLLGSSWGCG 20
                                                                                 7 Match 31.3%;
Local Similarity 55.0%;
Nes 11; Conservative
                                                                                                                                                                                                                                  7 LLIFSLVLSFVLGGSAQNCG
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Matches 11; Conserv
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Best Local Similarity
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A; Residues: 1-579 <WES>
                                                                                    Query Match
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                                                                                                                   Best Loca
Matches
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A;Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trad
A;Reference number: A71570; MUID:99000809; PMID:9784136
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F.1-10/Domain: signal sequence #status predicted <SIG>
F:22-43/Domain: propeptide #status predicted <PRO>
                                                                                                        A;Molecule type: DNA
A;Residues: 1-219 <ARN>
A;Cross-references: GB:AE001320; GB:AE001273; NID:g3328891; PIDN:AAC68062.1; PID:g332889
A;Experimental source: serotype D, strain UW-3/Cx
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  monofunctional biosynthetic peptidoglycan transglycosylase (EC 2.4.2.-) [imported] - Yez
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R; Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
A; Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A; Reference number: AB0001; MUID:21470413; PMID:11586360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chitinase (EC 3.2.1.14) (class II, acidic) precursor - sweet orange .
C;Species: Citrus sinensis (sweet orange)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C;Accession: T10106
R;Nairn, C,J; Niedz, R.P.; Hearn, C,J; Osswald, W.F.; Mayer, R.T.
Biochhim Biophys. Acte 1351, 22-26, 1997
A;Tille: CDNA cloning and expression of a class II acidic chitinase from sweet orange.
A;Reference number: Z16952; MUID:97236427; PMID:9116036
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A; Cross-references: GB:AL590842; PIDN:CAC92781.1; PID:g15981474; GSPDB:GN00175 C; Genetics:
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A; Residues: 1-292 <NAI>
A; Cross-references: EMBL: 270032; NID: 91220143; PIDN: CAA93847.1; PID: 91220144
A; Experimental source: cv. Valencia; callus
C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C:Species: Yersinia pestis
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 27-Nov-2001
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Pred. No. 23;
3; Mismatches 11; Indels
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Pred. No. 25;
1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 LSLTLSLVLLGSSWG------CGVPAITPALSYNQR 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pentosyltransferase
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                                                                                                                                                                                                                         C;Genetics:
A;Gene: yg6P
C;Superfamily: sugar nucleotide phosphorylase
                                                                                                                                                                                                                                                                                                                                    Query Match 31.3%;
Best Local Similarity 36.4%;
Matches 16; Conservative
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C,Keywords: glycosyltransferase;
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Matches 11; Conservative
                                                       A; Accession: B71511
A; Status: preliminary
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A; Status: preliminary
A; Molecule type: DNA
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R;West, C.E.; Waterworth, W.M.; Stephens, S.M.; Smith, C.P.; Bray, C.M. Plant J. 15, 221-229, 1998
A;Title: Cloning and functional characterisation of a peptide transporter expressed il A;Reference number: 215321; MUID:98388652; PMID:9721680
A;Accession: T04378
               C; Species: Rattus norvegicus (Norway rat)
C; Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C; Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C; Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C; Date: 16-Jul-1999 #sequence_revision 15000
R; Sekine, T.; Kusuhara, H.; Utsunomiya-Tate, N.; Tsuda, M.; Sugiyama, Y.; Kanai, Y.;
Biochem. Biophys. Res. Commun. 251, 586-591, 1998
A; Trieference number: JE0346; MUID:99011422; PMID:9792817
A; Reference number: JE0346
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A; Residues: 1-557 <SEK>
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C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000
C;Accession: T04378
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3; Mismatches
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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OM protein - protein search, using sw model

December 20, 2002, 15:12:58 ; Search time 9.04348 Seconds (without alignments) 1210.790 Million cell updates/sec Run on:

US-09-856-319B-4 1418 1 MLLLSLTLSLVLLGSSWGCG......AMYTRVSKFSTWINQVMAYN 264 Title: Perfect score: Sequence:

Scoring table:

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112892 seqs, 41476328 residues Searched:

Total number of hits satisfying chosen parameters:

112892

Minimum DB seq length: 0 . Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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-1- CATALYTIC ACTIVITY: Preferential cleavage: Tyr-i-Xaa, Trp-i-Xaa,
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MEDLINE-84170233; PubMed-6584866;
Pinsky S.D., Laforge K.S., Luc V., Scheele G.;
"Identification of cDMA clones encoding secretory isoenzyme forms: sequence determination of canine pancreatic prechymotrypsinogen 2
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Pred. No. 6.6e-102;
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-1- SUMILARITY: BELONGS TO PEPTIDASE FAMILY SI.
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13-AUG-1987 (Rel. 05, Last sequence update)
13-UNY-2002 (Rel. 14), Last annotation update)
Chymotrypsinogen 2 precursor (EC 3.4.21.1).
                                                                                                                                                                                                                                                                                                                                                                           263 AA
                                                           25; Mismatches
 BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PERMY PR00099; LTYPSIN; I.
PRINTS, PR00722; CHYMOTRYPSIN.
SMART; SM00020; TTYP_SPC; I.
PROSITE; PSS0240; TRYPSIN_DOM; I.
PROSITE; PS00134; TRYPSIN_HIS; I.
PROSITE; PS00135; TRYPSIN_HIS; I.
                                                                                                                                                                                                                                                                                      241 IQAPAMYTRVSKFSTWINQVMAYN 264
                                                                                                                                                                                                                                                                                                   241 VRAPAVYTRVSKFSTWINOVIAYN 264
           28002 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; K01173; AAA30841.1; -.
                                    89.28;
                                                  86.48;
                                                             Matches 228; Conservative
                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Canis familiaris (Dog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; A21195; A21195.
HSSP; P00766; IACB.
210 ;
264 AA;
                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEROPS; S01.152;
                                                                                                                                                                                                                                                                                                                                                                         CTR2_CANFA
P04813;
DISULFID
           SEQUENCE
                                     Query Match
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                                                                                                                                       61
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                                                  Best
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121 DLTLLKLASPARYTAQVSPVCLASTNEALPSGLTCVTTGWGRISGVGNVTPARLQQVVLP 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 LVTVNQCRQYWGARITDAMICAGGSGASSCQGDSGGPLVCQKGNTWVLIGIVSWGTKNCN 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGSLISPNWVVTAAHCQVTPGRHFVVLGEYDRSSNAEPVQVLSIARAITHPNWNANTMNN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MLLLSLTLSLVLLGSSWGCGVPAITPALSYNQRIVNGENAVPGSWPWQVSLQDNTGFHFC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg R.;
Submitted (MAR.2001) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: Preferential cleavage: Tyr-|-Xaa, Trp-|-Xaa, Phe-|-Xaa, Leu-|-Xaa, Location: Extracellular.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Digestion; Pancreas; Zymogen; Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Molecular cloning and nucleotide sequence of human pancreatic
                                                                                                                                                                                                                                                                                                                                                                                Length 263;
                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                           CHYMOTRYPSIN 2, A CHAIN.
CHYMOTRYPSIN 2, B CHAIN.
CHYMOTRYPSIN 2, C CHAIN.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                   2A2F449D813B3961 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
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Biochem. Biophys. Res. Commun. 158:569-575(1989)
                                            CHYMOTRYPSINOGEN 2.
                                                                                                                                                                                                                                                                                                                                                                                58.7%; Score 832.5; DB 1 57.2%; Pred. No. 1.9e-64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-AUG-1990 (Rel. 15, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Chymotrypsinogen B precursor (EC 3.4.21.1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               263 AA
                                                                                                                                                                                                                                                                                                                                                                                                         ; Pred. No. 1.9e
38; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 IQAPAMYTRVSKFSTWINQVMAYN 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            240 TSTPGVYARVTKLIPWVQQILQAN 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Pancreas;
MEDLINE-89134264; PubMed-2917002;
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                                                                                                                                                                                                                                                                                                                                 27787 MW;
  protease;
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                                            263
31
164
263
75
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                                                                                                                                                                                                                                                                                                                                   263 AA;
                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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Serine
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us-09-856-319b-4.rsp

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHYMOTRYPSIN B, A CHAIN.
CHYMOTRYPSIN B, B CHAIN.
CHYMOTRYPSIN B, C CHAIN.
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
                                                                                                                                                           Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
MARRY; SM00020; Tryp_SPc; 1.
PROSITE; PS50240, TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_BIS; 1.
PROSITE; PS00135; TRYPSIN_BIS; 1.
Hydrolase; Serine protease; Digestion; Pancreas; Zymogen; Signal.
                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 263;
                                                                                                                                                                                                                                                                                                                                                                                             74; Indels
                                                                                                                                                                                                                                                                                                                          ( SIMILARITY.
( SIMILARITY.
( SIMILARITY.
4C1C055A490B8701 CRC64;
                                                                                                                                                                                                                                        CHYMOTRYPSINGEN B.
                                                                                                                                                                                                                                                                                                                                                                          Score 822.5; DB 1 Pred. No. 1.4e-63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Chymotrypsin A precursor (EC 3.4.21.1).
Gadus morhua (Aliantic cod).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        263 AA
                                                                                                                                                                                                                                                                                                                                                                                             38; Mismatches
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SIMILARITY
                                                                                                                                                     Ser_protease_Try.
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                                                                                                                                           InterPro; IPR001314; Chymotrypsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 IQAPAMYTRVSKFSTWINQVMAYN 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 :| || || || || 240 TSSPGVYARVTKLIPWVQKILAAN 263
                                                                                                                                                                                                                                                                                                        87
87
87
87
                                                                                 EMBL; BC005385; AAH05385.1; -. PIR; A31299; A31299. HSSP; P00766; 1CHG.
                                                                                                                                                                                                                                                                                                                                                       27870 MW;
                                                                                                                                                                                                                                                                                                                                                                          58.0%;
                                                                         EMBL; M24400; AAA52128.1; -.
                                                                                                                                                                                                                                                                                                                                                                                             Matches 151; Conservative
                                                                                                              MEROPS; S01.152; -. Genew; HGNC:2521; CTRB1.
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                                                                                                                                                                                                                                                                                                        140
76
219
200
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31
164
263
75
75
213
                                                                                                                                                     IPR001254;
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                                                                                                                                                                                                                                                                                                                                                       263 AA;
                                                                                                                                MIM; 118890
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P47796;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Asgeirsson B., Bjarnason J.B.;
"Structural and kinetic properties of chymotrypsin from Atlantic cod (Gadus morhua). Comparison with bovine chymotrypsin.";
Comp. Blochem. Physiol. 99B:327-335(1991).
-!- CATALYTIC ACTIVITY: Preferential cleavage: Tyr-|-Xaa, Trp-|-Xaa, Phe-|-Xaa, Leu-|-Xaa.
-!- SUBCELULAR LOCATION: Extracellular.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
extinopteryyii; Neopteryyii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Paracanthopteryyii; Gadiformes; Gadidae; Gadus.
NCBL_TaxID-8049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12 LFRRTYGCGRPAISPVITGYSRIVNGEEAVPHSWSWQVSLQDQTGFHFCGGSLINENWVV
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(BY SIMILARITY).
(BY SIMILARITY).
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InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR001252; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPC; 1.
SMART; SM00020; TryP_SPC; 1.
PROSITE; PS00134; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_LISM; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
Hydrolase; Serine protease; Digestion; Pancreas; Zymogen; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Atlantic cod cDNA encoding a psychrophilic chymotrypsinogen.";
Biochim. Biophys. Acta 1219:211-214(1994).
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CHARGE RELAY SYS:
CHARGE RELAY SYS:
CHARGE RELAY SYS:
BY SIMILARITY.
BY SIMILARI
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38; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Pyloric caeca;
MEDLINE-92111252; PubMed-1764912;
                                                                                                                                                                                                                                                                                 TISSUE-Pyloric caeca;
MEDLINE-94368860; Pubmed-8086467;
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S; S01.152;
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79 TPGRHFVVLGEYDRSSNAEPVQVLSIARAITHPNWNANTMNNDLTLLKLASPARYTAQVS 138
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240 ETLAAN 245
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                      SEQUENCE, DISULFIDE BONDS, AND ACTIVE SITE.
MEDILE-68238908; bubMed=5649671;
Similite L.B., Furka A., Magabhushan N., Stevenson K.J., Parkes C.O.;
"Structure of chymotrypsinogen B compared with chymotrypsinogen A and
         132 RYTAQVSPVCLASTNEALPSGLTCVTTGWGRISGVGNVTPARLQQVVLPLVTVNQCRQYW 191
                                                 192 GARITDAMICAGGSGASSCQGDSGGPLVCQKGNTWVLIGIVSWGTKNCNIQAPAMYTRVS 251
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                                                                                                                                                                                                                                                                                                                       trypsinogen.";
Nature 218:343-346(1968)
-i- CATALYTIC ACTIVITY: Preferential cleavage: Tyr-|-Xaa, Trp-|-Xaa,
                                                                                                                                                                                                           Chymotrypsinogen B (EC 33.4.21.1).
Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
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-!-SURICELGULAR LOCATION: Extracellular.
-!-SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.
-!- DATABASE: NAME-Worthington enzyme manual;
WWW-*http://www.worthington-blochem.com/manual/C/CHY.html".
PIR; A00953; KYBOB.
HSSP; P00766; lACB.
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InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001324; Ser_protease_Try.
PR00122; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS50240; TRYPSIN_LDOM; 1.
PROSITE; PS00134; TRYPSIN_LIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
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57.7%; Pred. No. 1.6e-60;
iive 32; Mismatches 71;
                                                                                                                                                                             21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
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245 AA;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                              180 MICAGASGVSSCMGDSGGPLVCQKNGAWTLAGIVSWGSSTCSTSTPAVYARVTALMPWVQ 239
                                                                                                  139 PVCLASTNEALPSGLTCVTTGWGRISGVGNVTPARLQQVVLPLVTVNQCRQYWGARITDA 198
                                                                                                                                                                                                                                             199 MICAGGSGASSCQGDSGGPLVCQKGNTWVLIGIVSWGTKNCNIQAPAMYTRVSKFSTWIN 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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J. Biol. Chem. 259:14265-14270(1984).
-!- CATALYTIC ACTIVITY: Preferential cleavage: Tyr-|-Xaa, Trp-|-Xaa, Phe-|-Xaa, Leu-|-Xaa.
-!- SUBCELLULAR LOCATION: Extracellular.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
SIMILARITY).
SIMILARITY).
SIMILARITY).
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PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00135; TRYPSIN_LSE; 1.
Hydrolase; Serine protease; Digestion; Pancreas; Zymogen; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-85054881; Pubmed-6209274;
Bell G.I., Quinto C., Quiroga M., Valenzuela P., Craik C.S.
Rutter W.J.;
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CHYMOTRYPSIN B, B CHAIN.
CHYMOTRYPSIN B, C CHAIN.
CHARGE RELAY SYSTEM (BY SI
BY SIMILARITY.
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15-JUN-2002 (Rel. 41, Last annotation update)
Chymotrypsinogen B precursor (EC 3.4.21.1).
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InterPro; IPR001254; Ser_protease_Try.
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56CH;
66CH;
76CH;
16CT;
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16CB;
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1AFQ;
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                                                                                                                        1 MLLLSLTLSLVLLGSSWGCGVPAITPALSYNQRIVNGENAVPGSWPWQVSLQDNTGFHFC 60
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MEDLINE-67181721; PubMed-5971783;
Brown J.R., Hartley B.S.;
"Location of disulphide bridges by diagonal paper electrophoresis.
The disulphide bridges of bovine chymotrypsinogen A.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2012 (Boyline)
Bos taurus (Boyline).
Bos taurus (Boyline).
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Boyline; Boy
                                                                                                                                      181 LVTVNQCRQYWGARITDAMICAGGSGASSCQGDSGGPLVCQKGNTWVLIGIVSWGTKNCN
                                                                                                                                                                                                                                                           DITLLKLATPAGFSETVSAVCLPNVDDDFPPGTVCATTGWGKTKYNALKTPEKLQQAALP
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MEDILNE-67183948; PubMed-5972866;
Meloun B., Kluh I., Kostka V., Moravek L., Prusik Z., Vanacek J.,
Keil B., Sorm F.;
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                                                                   DB 1; Length 263;
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Blow D.M., Birktoft J.J., Hartley B.S.;
"Role of a buried acid group in the mechanism of action
                                          ACAFDBACF8C4DA6D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Amino-acid sequence of bovine chymotrypsinogen-A.";
Nature 201:1284-1287(1964).
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Biochim. Biophys. Acta 130:543-546(1966).
                                                        Score 781.5; DB 1;
Pred. No. 4.6e-60;
                                                                                                                                                                                                                                                                                                                                                                                                                                       245 AA.
              SIMILARITY.
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MEDLINE-67181723; PubMed-5971785;
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BY
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                                        27849 MW;
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53.8%;
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                                                                               Local Similarity 53.8
les 142; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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154
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263 AA;
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"Refined crystal structure of gamma-chymotrypsin at 1.9-A resolution. Comparison with other pancreatic serine proteases.";
J. Mol. Biol. 148:449-479(1981).
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MEDLINE=70177557; PubMed=5442169;
Freet S.T., Kraut J., Robertus J.D., Wright H.T., Xuong N.H.;
"Chymotrypsinogen: 2.5-A crystal structure, comparison with alpha-
chymotrypsin, and implications for zymogen activation.";
Biochemistry 9:1997-2009(1970).
                                                                                                              MEDLINE-72035052; PubMed-4399050; Birktoft J.J., Blow D.M., Henderson R., Steitz T.A.; "I. Serine proteinases. The structure of alpha-chymotrypsin."; Philos. Trans. R. Soc. Lond., B, Biol. Sci. 257:67-76(1970).
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MEDLINE-86011575; PubMed-4046030;
Tsukada H., Blow D.M.;
                                                                                                                                                                                                                                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF GAMMA-CHYMOTRYPSIN.
MEDLINE-82078042; PubMed-6914398;
Cohen G.H., Silverton E.W., Davies D.R.;
'Histidine sequences in the active centres of some 'serine'
                                         Biochem. J. 101:232-241(1966).
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6CHA; 16-OCT-87;
1CHG; 27-JAN-84;
1CHO; 16-JUL-88;
2GCH; 31-MAY-84;
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22-JUN-94.
22-JUN-94.
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                                                                                           X-RAY CRYSTALLOGRAPHY
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1-0CT-93.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2CGA; 15-APR-90.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2CHA; 31-MAY-84.
4CHA; 29-OCT-85.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-APR-94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-0CT-91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-APR-94
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79 TPGRHFVVLGEYDRSSNAEPVQVLSIARAITHPNWNANTMNNDLTLLKLASPARYTAQVS 138
                                                                          MICAGGSGASSCQGDSGGPLVCQKGNTWVLIGIVSWGTKNCNIQAPAMYTRVSKFSTWIN 258
                                                                                                                                                                                                                                                                                     TISSUE=Pyloric caeca;
MEDLINE-96439045; PubMed=8841380;
Leth-Larsen R., Asgeirsson B., Thorolfsson M., Noerregaard-Madsen M.,
                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Pyloric caeca;
MEDLINE-9211252; PubMed-1764912;
MEDLINE-9211252; PubMed-1764912;
ASSGLINE-9211252; PubMed-1764912;
"Structural and kinetic properties of chymotrypsin from Atlantic cod (Gadus morhua). Comparison with bovine chymotrypsin.";
Comp. Biochem. Physiol. 998:327-335(1991).
-:- CAMALYTIC ACTIVITY: Preferential cleavage: Tyr-1-Xaa, Trp-1-Xaa,
                                                                                                                                                                              01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1906 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Chymotrypsin B (EC 3.4.21.1).
Gadus morhua (Atlantic cod).
Gadus morhua (Atlantic rod).
Actinoperygii; Neopterygii; Teleostei; Euteleostei; Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Gadus.
NCTL_TaxID=8049;
                                         PVCLASTNEALPSGLTCVTTGWGRISGVGNVTPARLQQVVLPLVTVNQCRQYWGARITDA
                                                                                                                                                                                                                                                                                                                                                                                                         Hoch.

CATALYTIC A.
Phel-Taxa, Leu.,
1- SUBCELLULAR LOCATL.
1- SIMILARITY: BELONGS TO.
HSSP: PONT66; 1CHG.

MEROPS; S01.152;
DR InterPro; IPR001234; Ser_protease_Try.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PROSTE; PS00134; TRYPSIN.11.
DR PROSTE; PS00134; TRYPSIN.HIS; I.
DR PROSTE; PS00134; TRYPSIN.HIS; I.
DR PROSTE; PS00135; TRYPSIN.HIS; I.
DR PROSTE; PS00135; TRYPSIN.HIS; I.
DR PROSTE; PS00135; TRYPSIN.HIS; I.
DR PROSTE; PS00134; TRYPSIN.HIS; I.
DR PROSTE; PS00134; TRYPSIN.HIS; I.
DR PROSTE; PS00135; TRYPSIN.HIS; I.
DR PROSTE; PS00136; TRYPSIN.HISPIN.
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SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                          iochim. Biophys. Acta 1297:49-56(1996).
                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1-12 AND 16-31
                                                                                                                                                                         STANDARD;
                                                                                                                              240 OTLAAN 245
                                                                                                             259 QVMAYN 264
                                                                                                                                                                         CTRB_GADMO
P80646;
                                                                                                                                                                                                                                                                                                                   Hoejrup P.;
                                                                                                                                                                                                                                                                                                                                  morhua.";
                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                        RESULT 8
CTRB_GADMO
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     InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR001252; CHYMONTRYPSIN.
SMART; SM00020; Tryp_SPC; 1.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS00134; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00134; TRYPSIN_LISE; 1.
Hydrolase; Serine protease; Digestion; Pancreas; Zymogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 774.5; DB 1; Leuy...
Pred. No. 1.7e-59;
....+rhes 72; Indels
                                                                                          CHYMOTRYPSIN A, A CHAIN.
CHYMOTRYPSIN A, B CHAIN.
CHYMOTRYPSIN A, C CHAIN.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25666 MW; 91A9F28E2F3E3142 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54.6%;
57.3%;
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                                                                                            Query Match
Rest Local Similarity
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1 CGVPAIQPVLSGLSRIVNGEEAVPGSWPWQVSLQDKTGFHFCGGSLINENWVVTAAHCGV 60 CGVPAITPALSYNQRIVNGENAVPGSWPWQVSLQDNTGFHFCGGSLISPNWVVTAAHCQV 78

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[1]
SEQUENCE FROM N.A.
                                                                 MEROPS; S01.155;
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Matches 118;
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                                                                                         5
                                                                                                                                                                                61 RT-YHRVIVGEHDKASD-ENIQILKPSMVFTHPKWDSRTINNDISLIKLASPAVLGTNVS 118
                                                                                                                                                                                                                                PVCLASTNEALPSGLTCVTTGWG--RISGVGNVTPARLQQVVLPLVTVNQCRQYWGAR-I 195
                                                                                                                                                                                                                                                                  196 TDAMICAGGSGASSCQGDSGGPLVCQKGNTWVLIGIVSWGTKNCNIQAPAMYTRVSKFST 255
                                                                                                                                                                  79 TPGRHFVVLGEYDRSSNAEPVQVLSIARAITHPNWNANTMNNDLTLLKLASPARYTAQVS 138
                                                                                          Gaps
                                                                                                                CGVPAITPALSYNQRIVNGENAVPGSWPWQVSLQDNTGFHFCGGSLISPNWVVTAAHCQV 78
                                                                                                                                        1 CGSPAIQPQVTGYARIVNGEEAVPHSWPWQVSLQQSNGFHFCGGSLINENWVVTAAHCNV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -i- FUNCTION: ACTS UPON ELASTIN.
-i- CATALYTIC ACTIVITY: Preferential cleavage: Leu-i-Xaa, Met-i-Xaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and Phe-I-Xaa. Hydrolyzes elastin.
-- SUBCELULAR LOCATION: Secreted.
--- TISSUE SPECIFICITY: PANOREAS.
--- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. ELASTASE SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-87217962; PubMed-3646943;
Kawashima I., Tani T., Shimoda K., Takiguchi Y.;
Characterization of pancreatic elastase II cDNAs: two elastase II mRNAs are expressed in human pancreas.";
DNA 6:163-172(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE-88198076; Pubwed-2834346;
Shirasu Y., Yoshida H., Matsuki S., Takemura K., Ikeda N.,
Shimada Y., Ozawa T., Mikayama T., Iijima H., Ishida A., Sato Y.,
Tamai Y., Tanaka J., Ikenaga H.;
"Molecular cloning and expression in Escherichia coli of a cDNA
encoding human pancreatic clastase 2.";
J. Blochem. 102:1555-1563(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBL_TaxID=9823;
                                                               DB 1; Length 245;
                                                                                         Indels
QVT -> VIS (IN REF. 2).
S -> T (IN REF. 2).
PW -> Y (IN REF. 2).
74FE0D425517AB02 CRC64;
                                                                                         63;
                                                             Query Match 52.8%; Score 748.5; DB 1
Best Local Similarity 54.6%; Pred. No. 2.9e-57;
Matches 136; Conservative 43; Mismatches 63
                                                                                                                                                                                                                                                                                                                                                                                                                                 01-AUG-1988 (Rel. 08, Created)
101-AUG-1988 (Rel. 08, Last sequence update)
101-AUV-2002 (Rel. 41, Last annotation update)
Elastase 2 precursor (EC 3.4.21.71).
                                                                                                                                                                                                                                                                                                                                                                                                           269 AA.
 11
26
29
26260 MW;
                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
 9
26
28
245 AA;
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                                                                                                                                                                                                                                                                                                                    256 WINQVMAYN 264
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 CONFLICT
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TCGGTLVDQSWVLTAAHCISSSRTYRVVLGRHSLSTNEPGSLAVKVSKLVVHQDWNSNQL 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 119 N--NDLTLLKLASPARYTAQVSPVCLASTNEALPSGLTCVTTGWGRISGVGNVTPARLQQ 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26
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SIMILARITY).
SIMILARITY).
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 LLLSLTLSLVLLGSSWGCGVPAITPALSYNQRIVNGENAVPGSWPWQVSLQ-DNTG--FH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16;
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C -> S (IN REF. 2).

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S -> Y (IN REF. 2).

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W; BACGFE69AF4DDE56 CRC64;
                                                                                                                                                                                                                                                                              ACTIVATION PEPTIDE
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Similarity 43.1%; Score 537; DB 1;
Similarity 43.1%; Pred. No. 4.5e-39;
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                                                                                                                                                             SMARY; SM00020; Tryp_SPC; 1.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
HYGIOLASE; Serine protease; Zymogen; Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SWGTK-NCN-IQAPAMYTRVSKFSTWINQVMAYN 264
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Interpro; IPR001254; Ser_protease_Try.
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28699 MW;
                                                                                                                            Pfam; PF00089; trypsin; 1. PRINTS; PR00722; CHYMOTRYPSIN.
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EMBL; M16651; AAA31027.1;
EMBL; D00237; BAA00166.1;
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                                  PIR; A26823; A26823.
HSSP; P00763; 1DPO.
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11;

271 AA

PRT;

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STANDARD;
                                                                                                                                                                                                                                                                                                                              pancreas.";
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                                                                                                                                                                                   between the Swiss Institute of Bioinformatics and the EMBL outstation—
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entities requires a license agreement (see http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration
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                   119 --NNDLTLLKLASPARYTAQVSPVCLASTNEALPSGLTCVTTGWGRISGVGNVTPARLQQ 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59 FCGGSLISPNWVVTAAHCQVTPGRHFVVLGEYDRSSNAEPVQVLSIARAITHPNWNANTM 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        117 AQGNDIALLKLASSVPLTDKIQLGCLPAAGTILPNNYVCYVTGWGRLQSNG-ALPDILQQ 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 177 VVLPLVTVNQCR--QYWGARITDAMICAGGSG-ASSCQGDSGGPLVCQKGN-TWVLIGIV
                                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY.
ACTIVATION PEPTIDE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98; Indels
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InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00089; Lrypsin, 1.
PRINTS: PR00722; CHYMOTRYPSIN.
SWART; SW00020; Tryp_SPc; 1.
PROSITE; PS00134; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_LIS; 1.
PROSITE; PS00135; TRYPSIN_EBR; 1.
PROSITE; PS00135; TRYPSIN_EBR; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     ELASTASE
           MEDLINE-98079203; PubMed-9418008;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28856 MW;
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269
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121
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SIGNAL
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RESULT 11 EL2_RAT

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                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                           J. Biol. Chem. 259:14271-14278(1984).
-!- FUNCTION: ACTS UPON ELASTIN.
-!- CATALYTIC ACTIVITY: Preferential cleavage: Leu-|-Xaa, Met-|-Xaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and Phe-1-Xaa. Hydrolyzes elastin.
-!- SUBCELULAR LOCATION: Secreted.
-!- TISSUE SPECIFUCITY: PANCREAS.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. ELASTASE SUBFAMILY.
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SIMILARITY).
SIMILARITY).
                                                                                                                                                                                                                                            "Primary structure of two distinct rat pancreatic preproelastases determined by sequence analysis of the complete cloned messenger ribonucleic acid sequences.";
                                                                                                                                                                                                                                                                                                                                                                                               rat
                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDIJNE=85054882; PubMed=6094548;
Swift G.H., Craik C.S., Stary S.J., Quinto C., Lahaie R.G.,
Rutter W.J., Macdonald R.J.;
"Structure of the two related elastase genes expressed in the
                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE-82182967; PubMed-6918221;
McDonald R.J., Swift G.H., Quinto C., Swain W., Pictet R.L.,
Nikovits W., Rutter W.J.;
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CHARGE RELAY SYSTEM
CHARGE RELAY SYSTEM
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                        21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Elastase 2 precursor (EC 3.4.21.71).
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SIGNAL 1
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InterPro; IPR001254; Ser_protease_Try.
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EMBL; L00118; AAA98780.1; JOINED.
EMBL; L00119; AAA98780.1; JOINED.
EMBL; L00120; AAA98780.1; JOINED.
EMBL; L00121; AAA98780.1; JOINED.
EMBL; L00121; AAA98780.1; JOINED.
EMBL; L00123; AAA98780.1; JOINED.
PIR; A00961; ELRTZ.
HSSP; P00772; IELG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PRO0722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS550240; TRYPSIN_DOM; 1.
PROSITE; PS00114; TRYPSIN_HIS; 1.
PROSITE; PS001135; TRYPSIN_HIS; 1.
                                                                                                                                                                                                                                                                                                 Biochemistry 21:1453-1463(1982).
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                                                                                                          Rattus norvegicus (Rat)
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75
123
218
218
224
245
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NCBI_TaxID=10116;
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EL3B_HUMAN
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ACT_SITE
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EL3B_HUMAN
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TISSUE-Pancreas;
MEDILINE-88198076; PubMed-2834346;
Shirasu Y., Yoshida H., Matsuki S., Takemura K., Ikeda N., Shimada Y.,
Ozawa T., Mikayama T., Iljima H., Ishida A., Sato Y., Tamai Y.,
                                                                                                                                                                       118 LSNGNDIALVKLASPVALTSKIQTACLPPAGTILPNNYPCYVTGWGRLQTNG-ATPDVLQ 176
                                                                                                                                                                                                          176 QVVLPLVTVNQC -- RQYWGARITDAMICAGGSG-ASSCQGDSGGPLVCQKGN-TWVLIGI 231
                                                                                                                      Gaps
                                                                                                          HFCGGSLISPNWVVTAAHCQVTPGRHFVVLGEYDRSSNAEPVQVLSIARAITHPNWNANT 117
                                                                           2 LLLSLTLSLVLLGSSWGCGVPAITPALSYN-QRIVNGENAVPGSWPWQVSLQ---DNTGF 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kawashima I., Tani T., Shimoda K., Takiguchi Y.;
"Characterization of pancreatic elastase II cDNAs: two elastase II mRNAs are expressed in human pancreas.";
                                                                                                                                                  MN--NDLTLLKLASPARYTAQVSPVCLASTNEALPSGLTCVTTGWGRISGVGNVTPARLQ
                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-88107665; PubMed-3427074;
Fletcher T.S., Shen W.F., Largman C.;
Primary structure of human pancreatic elastase 2 determined by sequence analysis of the cloned mRNA.";
Biochemistry 26:7256-7261(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tanaka J., Ikenaga H.;
"Molecular cloning and expression in Escherichia coli of a cDNA
encoding human proteatic elastase 2.";
J. Biochem. 102:1555-1563(1987).
                       Length 271;
                                            100; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to the EMBL/GenBank/DDBJ databases
 125C783B857B71E3 CRC64;
                    36.5%; Score 517; DB 1;
41.1%; Pred. No. 2.4e-37;
tive 46; Mismatches 100
                                                                                                                                                                                                                                                                                                                EL2A_HUMAN STANDARD; PRT; 269 AA. P08217; 014243; 01-AUG-1988 (Rel. 08, Created) LAUG-1988 (Rel. 08, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                    232 VSWG-TKNCNI-QAPAMYTRVSKFSTWINQVMAYN 264
                                                                                                                                                                                                                                                                                                                                                                     Elastase 2A precursor (EC 3.4.21.71).
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata
Mammalia; Eutheria; Primates; Catarrh
                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-87217962; PubMed-3646943;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1- FUNCTION: ACTS UPON ELASTIN.
 28885 MW;
                                            Conservative
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271 AA;
                               Local Similarity
es 113; Conserv
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  SEQUENCE
                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N--NDLTLLKLASPARYTAQVSPVCLASTNEALPSGLTCVTTGWGRISGVGNVTPARLQQ 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SKGNDIALLKLANPVSLTDKIQLACLPPAGTILPNNYPCYVTGWGRLQTNGAV-PDVLQQ 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            177 VVLPLVTVNQCRQ--YWGARITDAMICAGGSGA-SSCQGDSGGPLVCQKGN-TWVLIGIV 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59 FCGGSLISPNWVVTAAHCQVTPGRHFVVLGEYDRSSNAEPVQVLSIARAITHPNWNANTM 118
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CHARGE RELAY SYSTEM (BY SIMILARITY).
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C -> V (IN REF. 3).
C -> V (IN REF. 3).
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  cleavage: Leu-|-Xaa, Met-|-Xaa
                                                                                            S1. ELASTASE SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16;
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ELASTASE 2A.
BY SIMILARITY.
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Pred. No. 3.5e-37;
                    and Phe-1-Xaa. Hydrolyzes elastin.
--- SUGEELLULAR LOGATION: Secreted.
--- TISSUE SPECIFICITY: PANCREAS.
--- SIMILARITY: BELONGS TO PEPTIDASE FAMILY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001254; Ser_protease_T
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_HIS; 1.
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                                                                                                                                                                                                                                                                                                                              EMBL, M16631; AAA52374.1; -. BMBL, M16652, AA55280.1; -. EMBL, D00236; BAA010165.1; -. EMBL, AL512883; CAC42421.1; -. EMBL, R2C070731, AAH07031.1; -. PIR; B26823; B26823.
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CATALYTIC ACTIVITY:
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202
243
73
121
216
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Genew; HGNC:15945; ELA3B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Pancreas;
MEDLINE-8928996; PubMed-2737288;
Wendorf P., Geyer R., Sziegoleit A., Linder D.;
"Localization and characterization of the glycosylation site of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hydrolyse elastin.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. ELASTASE SUBFAMILY.
-!- CAUTION: Was originally (Ref.5) thought to be elastase 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pancreatic elastase 1.";
FEBS Lett. 249:275-278(1989).
-!- FUNCTION: EFFICIENT PROTEASE WITH ALANINE SPECIFICITY BUT ONLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LITTLE ELASTOLYTIC ACTIVITY.
                                                                                            Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                             Shen W., Fletcher T.S., Largman C.; "Primary structure of human pancreatic protease E determined by sequence analysis of the cloned mRNA."; Biochemistry 26:3447-3452(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDINE-19325560, PubMed-2753124;
Moulard M., Kerfelec B., Mallet B., Chapus C.;
Moulard M., Rorfelec B., Mallet B., Chapus C.;
"Identification of a procarboxypeptidase A-truncated protease binary complex in human pancreatic juice.";
FEBS Lett. 250:166-170(1989).
                                                                                                                                                            TISSUE-Pancreas;
MEDLINE-88087253; PubMed=2826474;
MEDLINE-88087253; PubMed K., Takiguchi Y.;
Tani T., Obsumi J., Mita K., Takiguchi Y.;
Tidentification of a novel class of elastase isozyme, human pancreatic elastase III, by cDNA and genomic gene cloning.";
J. Biol. Chem. 263:1231-1239(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 94-164, AND CARBOHYDRATE-LINKAGE SITES ASN-114.
                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                    Strausberg R.; Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
            01-NOV-1988 (Rel. 09, Created)
16-CT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Elastase IIIB precursor (EC 3.4.21.70) (Protease E).
                                                                                                                                                                                                                                                                                                                                                      MEDLINE-88000545; PubMed-3477287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL, BC005216, AAH05216.1; -. EMBL, M18692, AAA58454.1; -. PIR, B29934, B29934.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M16630; AAA36482.1; -.
EMBL; BC005216; AAH05216.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GlycoSuiteDB; P08861; -. SWISS-2DPAGE; P08861; HUMAN.
                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 4-270 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; S04999; S04999.
PIR; S04490; S04490.
HSSP; P05805; lFON.
                                                                                Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 31-50.
                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEROPS; S01.205;
                                                                                                                                                                                                                                                                           TISSUE-Pancreas;
                                                                                                                        NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Pancreas;
                                                                                                                                                                                                                                                                                                                                           TISSUE-Pancreas;
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59 FCGGSLISPNWVVTAAHCQVTPGRHFVVLGEYDRSSNAEPVQVLSI--ARAITHPNWNAN 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57 TCGGSLIAPDWVVTAGHCISSSWTYQVVLGEYDRAVKEGPEQVIPINSGDLFVHPLWNRS 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        175 QQVVLPLVTVNQCRQ--YWGARITDAMICAGGSGASSCQGDSGGPLVC-QKGNTWVLIGI 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 176 QEALLPVVDYEHCSRWNWWGSSVKKTMYCAGGDIRSGCNGDSGGPLNCPTEDGGWQVHGV 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       117 TM--NNDLTLLKLASPARYTAQVSPVCLASTNEALPSGLTCVTTGWGRISGVGNVTPARL 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 LLLSLTLSLVLLGSSWGCGVPAITPALSYNQRIVNGENAVPGSWPWQVSLQ-DNTG--FH 58
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15-DEC-1998 (Rel. 37, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
Proproteinase E precursor (Procarboxypeptidase A complex component III) (Procarboxypeptidase A-S6 subunit III) (PROCPA-S6 III)
Bos taurus (Bovine).
                                                                                                                                                                                                                                                     SIMILARITY).
SIMILARITY).
SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               117 CVACGNDIALIKLSRSAQLGDAVQLASLPPAGDILPNETPCYITGWGRLYTNGPL-PDKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-25.
MEDLINE-91099520; PubMed-2269366;
Pascual R., Vendrell J., Aviles F.X., Bonicel J., Wicker C.,
                                                                                                                                                                                          OR 16 (POTENTIAL). ACTIVATION PEPTIDE (POTENTIAL).
                                                         PRINTS; PRO0722; CHYMOTRYPDIN.
SMART; SM00020; Tryp_SPC; 1.
SMOSITE; PS50240; TRYPSIN_LOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
Hydrolase; Serine protease; Zymogen; Signal; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                  DISTRIBUTION

PROBABLE.

BY SIMILARITY.

BY SIMILARITY.

N-LINKED (GICNAC. ..).

/FTIG=CAR.000212.

R -> G (IN REF. 3).

M -> R (IN REF. 3).

MISSING (IN REF. 5).

MISSING (IN REF. 5).

MISSING (IN REF. 5).

MISSING (IN REF. 5).

W; B14BE0AAD3695AFE CRC64;
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CHARGE RELAY SYSTEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36.2%; Score 513.5; DB 1
11arity 41.4%; Pred. No. 4.7e-37;
Conservative 46; Mismatches 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        253 AA
                                                                                                                                                                                                                                 ELASTASE IIIB.
                                                                                                                                                                                                                                                                                                                     BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          232 VSW-GTKNCNI-QAPAMYTRVSKFSTWINQVMA 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |: | | : | : | | : | 236 TSFVSAFGCNTRRKPTVFTRVSAFIDWIEETIA 268
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00089; trypsin; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    164 R
29293 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64
79
131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          270 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best_Local Similarity
Matches 113; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64
79
129
164
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P05805;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONFLICT
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                                                                                                                                                                                            SIGNAL
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Spins . W. Mar

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               "Autolysis of proproteinase E in bovine procarboxypeptidase A ternary complex gives rise to subunit III."; FEBS Lett. 277:37-41(1990).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGGSGASSCQGDSGGPLVCQKGN-TWVLIGIVSW-GTKNCN-IQAPAMYTRVSKFSTWIN 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GEYDRS -- SNAEPVQVLSIARAITHPNWNANTM -- NNDLTLLKLASPARYTAQVSPVCLA 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         144 STNEALPSGLTCVTTGWGRISGVGNVTPARLQQVVLPLVTVNQCRQ--YWGARITDAMIC 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31 NORIVNGENAVPGSWPWQVSLQ---DNTGFHFCGGSLISPNWVVTAAHCQVTPGRHFVVL 87
                                                                                                                                                                                                        ENVIRONMENT OF THE RUMINANT DUODENUM.
SUBUNIT: HETEROTRIMER OF SUBUNIT III; CARBOXYPEPTIDASE A AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Venot N., Sclaky M., Pulgerver A., Desnuelle P., Laurent G., "Amino acid sequence and disulfide bridges of subunit III, a defective endopeptidase present in the bovine pancreatic 6 S procarboxypeptidase A complex.";

Eur. J. Blochem. 157:91-99(1986).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27337 MW; 24663724D8AE409C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35.5%; Score 503.5; DB 1
43.5%; Pred. No. 3.1e-36;
tive 37; Mismatches 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                             \mathbf{s}_{1}
                                                                                                                                                                                                                                                                                                                                                                                                                        -1- SUBCELLUIAR LOCATION: EXTRACELLULAR.
-1- TISSUE SPECIFICITY: PANCREAS.
-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY
                                                                               14-253, AND DISULFIDE BONDS.
                                                                                               MEDLINE-86220198; PubMed-3519215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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57
103
206
187
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PDB; 1FON; 14-OCT-96.
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100
140
171
196
253 AA;
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248 ETIASN 253
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Matches 107;
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RRARE RRAFE RRARE 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACTIVITY.
--- CATALYITY: Preferential cleavage: Leu-|-Xaa, Tyr-|-Xaa, Phe-|-Xaa, Met-|-Xaa, Trp-|-Xaa, Gln-|-Xaa, Asn-|-Xaa.
--- TISSUE SPECIFICITY: PANCREAS.
--- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. ELASTASE SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-98207038; PubMed-9538241;
Yoshino-Yasuda I., Kobayashi K., Akiyama M., Itoh H., Tomomura A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "A human pancreatic chymotrypsin: biochemical and molecular characterization.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nolkura T., Saheki T.;
"Molecular cloning and expression of human caldecrin.";
FEBS Lett. 386:26-28(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                        09995; Q9NUH5; 000765; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) 16-OCT-2001 (Rel. 40, Last annotation update) 16-OCT-COO1 (Rel
     268 AA
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InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00089; trypsin: 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SWART; SW00020; Tryp_SPC; 1.
PR0SITE; PS50240, TRYPSIN_LDOM; 1.
PROSITE; PS00114; TRYPSIN_LIS; 1.
PROSITE; PS001135; TRYPSIN_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [1]
SEQUENCE FROM N.A., AND VARIANT TRP-80.
     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Pancreas;
MEDLINE=96221265; PubMed=8635596;
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EMBL, Y13697, CAA74031.1; -.
HSSP; P00766; 1CHG.
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STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEROPS; S01.157; -.
Genew; HGNC:2523; CTRC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
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     CLCR_HUMAN
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Hydrolase; Serine protease; Glycoprotein; Zymogen; Signal;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                             POTENTIAL.

ACTIVATION PEPTIDE.
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N'LINKED (GLCNAC. ..) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  235 GT-KNCNI-QAPAMYTRVSKFSTWINQVM 261
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52 N
29484 MW;
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52
268 AA;
                                Polymorphism.
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Search completed: December 20, 2002, 15:17:13 Job time : 10.0435 secs

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December 20, 2002, 15:14:28; Search time 16.6957 Seconds (without alignments) 1520.126 Million cell updates/sec
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1418
1 MLLESLTLSLVLLGSSWGCG......AMYTRVSKFSTWINQVMAYN 264
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                           283224 seqs, 96134422 residues
                                                                            OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                     BLOSUM62
Gapop 10.0 , Gapext 0.5
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Perfect score:
Sequence:
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                                                                                                              Run on:
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries . Minimum DB seq length: 0 Maximum DB seq length: 2000000000

283224

Total number of hits satisfying chosen parameters:

PIR_73:* Database :

1: pirl:* 2: pir2:* 3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	-; '	7	chymotrypsin (EC 3	chymotrypsin (EC 3	<u>임</u>	_	SE SE	) E	chymotrypsin B - A	pancreatic elastas	pancreatic elastas	pancreatic elastas		polyprotein - Afri	pancreatic elastas	pancreatic elastas		Ω.	pancreatic elastas	plasmin (EC 3.4.21	plasmin (EC 3.4.21	tic e	chymotrypsin-like	plasmin (EC 3.4.21		plasmin (EC 3.4.21	$\overline{}$	~	prostasin (EC 3.4.	plasmin (EC 3.4.21
SUMMARIES		138130	A21195	A31299	S47537 ·	KYBOB	KYRTB	KYBOA	S72219	A26823	ELRT2	B26823	B29934	T30337	S68826	S68825	A25528	CPBOA3	A29934	PLMS	PLHU	C26823	A23473	B61545	B30848	PLPG	S56160	A47246	01	A61545
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RESULT 2 A21195

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TRRT1 JQ1473	TRPGTR JC4171	ELRT1 TRRT2	A32410	14626U TRDGC	PLBO A47547	TRDG	A38654	S0065/ A43090	A32869
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246 268	231 274	266	275	246	812 786	247	276	1035	1420
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454.5	447	444	443.5	443	441.5	440.5	440.5	440.5	439
30	32 33	34 35	36	38	39 40	41	42	4 4	45

# ALIGNMENTS

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C.Species: Gadus morrhua (Atlantic cod)
C.Date: 26-Dec-1994 #sequence_revision 03-Aug-1995 #text_change 22-Jun-1999
C.Date: 26-Dec-1994 #sequence_revision 03-Aug-1995 #text_change 22-Jun-1999
C.Accession: 847537; 843163
R.Gudmundsdottir, A.; Oskarsson, S.; Eakin, A.E.; Craik, C.S.; Bjarnason, J.B.
Biochim. Biophys. Acta 1219, 211-214, 1994
A.Title: Atlantic cod cDNA encoding a psychrophilic chymotrypsinogen.
A.Reference number: 847537; MUID:9436860; PMID:8086467
A.Accession: 847537
A.Molecule type: mRNA
A.Residues: 1-263 <GUDD
A.Cross-references: EMBL:X78490; NID:9468750; PIDN:CAA55242.1; PID:9468751
C.Superfamily: trypsin homology
C.Superfamily: trypsin homology
C.Superfamily: trypsin digestion; serine proteinase
F:19-263/Product: Chymotrypsin #status predicted <AMAT>
F:34-256/Domain: trypsin homology <ARAT>
F:75,120,213/Active site: His, Asp, Ser #status predicted
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N;Alternate names: chymotrypsinogen B
C;Species: Bos primigenius taurus (cattle)
C;Bate: 08-0ct-1981 #sequence_revision 08-oct-1981 #text_change 18-Jul-1997
C;Accession: A00953
R;Smillie, L.B.; Furka, A.; Nagabhushan, N.; Stevenson, K.J.; Parkes, C.O.
                                                                                         GGSLISEDWVVTAAHCGVRTS-DVVVAGEFDQGSDEENIQVLKIAKVFKNPKFSILTVNN 119
                                                                                                                                                                                                                                                                                                     72 TAAHCQVTPGRHFVVLGEYDRSSNAEPVQVLSIARAITHPNWNANTMNNDLTLLKLASPA 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12 LLGSSWGCGVPAITPALSYNQRIVNGENAVPGSWPWQVSLQDNTGFHFCGGSLISPNWVV 71
                                                                                                                                                                                              1 MAFLWLLSCWALLGTTFGCGVPAIHPVLSGLSRIVNGEDAVPGSWPWQVSLQDKTGFHFC
                                                              DLTLLKLASPARYTAQVSPVCLASTNEALPSGLTCVTTGWGRISGVGNVTPARLQQVVLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  precursor - Atlantic cod
                                                                                                                                                                                                                                                                                                                                                                                                               240 TSSPGVYARVTKLIPWVQKILAAN 263
                                                                                                                                                                                                                                                                                                                                                                               241 IQAPAMYTRVSKFSTWINQVMAYN 264
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C; Species: Homo sapiens: (man)
C; Species: Homo sapiens: (man)
C; Date: 08-Jun-1989 #sequence_revision 08-Jun-1989 #text_change 22-Jun-1999
C; Accession: A31299
R; Tomita, N.; Izumoto, Y.; Horii, A.; Doi, S.; Yokouchi, H.; Ogawa, M.; Mori, T.; Matsub Biochem. Biophys. Res. Commun. 158, 569-575, 1989
A; Title: Molecular cloning and nucleotide sequence of human pancreatic prechymotrypsinog A; Reference number: A31299; MUID:89134264; PMID:2917002
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chymotrypsin (EC 3.4.21.1) 2 precursor - dog
C;Species: Canis lupus familiaris (dog)
C;Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 22-Jun-1999
C;Accession: A21195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 DLTLLKLASPARYTAQVSPVCLASTNEALPSGLTCVTTGWGRISGVGNVTPARLQQVVLP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGSLISPNWVVTAAHCQVTPGRHFVVLGEYDRSSNAEPVQVLSIARAITHPNWNANTMNN 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                       R.Pinsky, S.D.; LaForge, K.S.; Luc, V.; Scheele, G.
Proc. Natl. Acad. Sci. U.S.A. 80, 7486-7490, 1983
ArTitle: Identification of cDNA clones encoding secretory isoenzyme forms A; Reference number: A21195; MUID:84170253; PMID:554866
A; Accession: A21195
A; Mulcule type: mRNA
A; Residues: 1-263 < PIN>
A; Residues: 1-263 < PIN>
A; Residues: 1-263 < PIN>
A; Cross-references: GB:K01173; NID:g163945; PIDN:AAA30841.1; PID:g163946
C; Superfamily: trypsin trypsin homology
C; Keywords: hydrolase; protein d1gestion; serine proteinase
F; 34-256/Domain: trypsin homology < RXP>
F; 75, 120, 213/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:M24400; NID:g181189; PIDN:AAA52128.1; PID:g181190 C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 LVTVNQCRQYWGARITDAMICAGGSGASSCQGDSGGPLVCQKGNTWVLIGIVSWGTKNCN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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A;Map position: 16q23.1-16q23.1
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; protein digestion; serine proteinase
F;34-256,Domain: trypsin homology C;Key Cyclomain: Trypsin homology 
F;75,120,213/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58.7%; Score 832.5; DB 2
57.2%; Pred. No. 1.3e-61;
Live 38; Mismatches 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chymotrypsin (EC 3.4.21.1) precursor - human
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Best Local Similarity 57.29
Matches 151; Conservative
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Matches 151; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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A;Molecule type: mRNA
A;Residues: 1-263 <TOM>
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GGSLISPNWVVTAAHCQVTPGRHFVVLGEYDRSSNAEPVQVLSIARAITHPNWNANTMNN 120
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A;Title: Structure of chymotrypsinogen B compared with chymotrypsinogen A and trypsinogen A;Reference number: A00953; MUD: 68238908; PMID: 5649671
A;Reference number: A00953; MUD: 68238908; PMID: 5649671
A;Reference number: A00953
A;Reference number: A00953
A;Residues: 1-245 <SMID>
C;Comment: D;Pymotrypsinogen B.is synthesized, along with chymotrypsinogen A, in the acir C;Comment: Chymotrypsinogen B.is synthesized, along with chymotrypsinogen A, in the acir C;Comment: The first activation cleavage, leading to pi-chymotrypsin B, occurs in the sa C;Superfamily: trypsin; trypsin homology
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; pnorteas; protein digestion; serine proteinase; zymogen F;1-15,700main: propeptide #status experimental <PRO>
F;16-2345/Poomain: trypsin homology <PRO>
F;16-2345/Domain: trypsin homology <PRO>
F;11-122,42-58,136-201,168-182,191-220/Pisulfide bonds: #status experimental
F;57,102,195/Active site: His, Asp, Ser #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Sections: Nature norvegicus (Norway rat.)
C; Sections: Nature norvegicus (Norway rat.)
C; Accession: A22658
K; Bell, G.I.; Oulinto, C.; Oulinto, Oulinto, C.; Oulinto, Ouli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ï
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 AVCLPSADEDFPAGMLCATTGWGKTKYNALKTPDKLQQATLPIVSNTDCRKYWGSRVTDV 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PVCLASTNEALPSGLTCVTTGWGRISGVGNVTPARLQQVVLPLVTVNQCRQYWGARITDA 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MICAGGSGASSCQGDSGGPLVCQKGNTWVLIGIVSWGTKNCNIQAPAMYTRVSKFSTWIN 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19 CGVPAITPALSYNQRIVNGENAVPGSWPWQVSLQDNTGFHFCGGSLISPNWVYTAAHCQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79 TPGRHFVVLGEYDRSSNAEPVQVLSIARAITHPNWNANTMNNDLTLLKLASPARYTAQVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55.5%; Score 786.5; DB 1;
1larity 57.7%; Pred. No. 8e-58;
Conservative 32; Mismatches 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chymotrypsin (EC 3.4.21.1) B precursor - rat
N;Alternate names: chymotrypsinogen B
C;Species: Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match
Best Local Similarity 53.8 Matches 142; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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ETLAAN 245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Sim
Matches 142;
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A,Title: Location of disulphide bridges by diagonal paper electrophoresis. The disulp A; Reference number: A90235; MUID:67181721; PMID:5971783
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A;Title: Salective oxidation of Met-192 in bovine alpha-chymotrypsin. Effect on catal A;Reference number: $29650; MUID:93160238; PMID:8431470
A;Reference number: $29650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Comment: Chymotrypsinogens are synthesized in the acinar cells of pancreas.
C;Comment: Tryptic cleavage after Arg-15 results in a fully active enzyme (pl-chymotr C;Comment: Tryptic cleavage after Arg-15 results in a fully active enzyme (pl-chymotr dela-chymotrypsin; further chymotryptic cleavage liberates the dipeptide Thr-147 and Asn-148 directly from chymotrypsinogen, which leads to the degraded form neochymotr C;Superfamily: trypsin chymotrogy
C;Seyworfamily: trypsin chymotrypsinogen
F;1-245/Product: chymotrypsinogen #status experimental <2YM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Z.; Vanacek, J.; Keil, B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A Molecule type: protein
A, Residues: 1-101, N', 103-245 < BRO>
A; Residues: 1-101, N', 103-245 < BRO>
R: Blow, D.M.; Birktoft, J.J.; Hartley, B.S.
Nature 221, 337-340, 1969
A; Title: Role of a buried acid group in the mechanism of action of chymotrypsin.
A; Reference number: A91158; MulD: 69106266; PMID: 5764436
A; Contents: annotation; revision to residue 102
B; Meloun, B.; Kluh, I.; Kostka, V.; Moravek, L.; Prusik, Z.; Vanacek, J.; Keil, 18 blochim: Blophys. Acta 130, 543-346, 1966
A; Title: Covalent structure of bovine chymotrypsinogen A.
A; Reference number: A90572; MulD: 67183948; PMID: 5972866
A; Accession: A91158
A; Molecule type: protein
A; Residues: 1-101, N', 103-245 < MEL>
A; Note: disulfide bonds were determined
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A.Residues: 1-12;16-27;149-160;181-200 <CUT>
R:Smillie, L.B.; Hartley, B.S.
Biochem. J. 101, 232-241, 1966
A.Title: Histidine sequences.in the active centres of some 'serine' proteinases. A:Reference number: A90236; MUID:67181723; PMID:5971785
A.Contents: annotation; active site
R:Birktoft, J.J.; Blow, D.M.; Henderson, R.; Steitz, T.A.
Philos. Trans. R. Soc. Lond. B257, 67-76, 1970
A:Title: The structure of alpha-chymotrypsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chymotrypsin (EC 3.4.21.1) A precursor - bovine
N'Alternate names: chymotrypsinogen A
C.Species: Bos primigenius taurus (cattle)
C.Species: Bos primigenius taurus (cattle)
C.Species: 07-May-1981 #sequence_revision 07-May-1981 #text_change 07-May-1999
C.Specession: A90235, A93158; S29650; A00952
B.S.Brown, J.R.; Hartley, B.S.
Biochem. J. 101, 214-228, 1966
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F;1-122,42-58,136-201,168-182,191-220/Disulfide bonds: #status experimental
F;57,102,195/Active site: His, Asp, Ser #status experimental
180
                                                                                                                                                                                     181 LVTVNQCRQYWGARITDAMICAGGSGASSCQGDSGGPLVCQKGNTWVLIGIVSWGTKNCN 240
                                                                                                                                                                                                                                                                                                                                                                      DLTLLKLASPARYTAQVSPVCLASTNEALPSGLTCVTTGWGRISGVGNVTPARLQQVVLP
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A;Contents: annotation; X-ray crystallography
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 IQAPAMYTRVSKFSTWINQVMAYN 264
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Matches 118;
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                                                                                                                                                                                                                                                                                                                                                                                                                   chymotrypsin B - Atlantic cod (fragments)

C;Species: Gadus morhua (Atlantic cod)

C;Species: Gadus morhua (Atlantic cod)

C;Date: 19-War-1998 #sequence_revision 17-Apr-1998 #text_change 07-Aug-1998

C;Accession: S7219

R;Leth-Larsaen, R; Asgeirsson, B.; Thororlfsson, M.; Norregaard-Madsen, M.; Hojrup, Blochim. Biophys. Acta 1297, 49-56, 1996

A;Title: Structure of chymotrypsin variant B from Atlantic cod, Gadus morhua.

A;Reference number: S72219; MUID:96439045; PMID:8841380

A;Accession: S72219

A;Status: preliminary
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9
                                                                                                                                            TIS-DVVVAGEFDQGSSSEKIQKLKIAKVFKNSKYNSLTINNDITLLKLSTAASFSQTVS 119
                                                                                                                                                                                                        TPGRHFVVLGEYDRSSNAEPVQVLSIARAITHPNWNANTMNNDLTLLKLASPARYTAQVS 138
                                                                                                                                                                                      PVCLASTNEALPSGLTCVTTGWGRISGVGNVTPARLQQVVLPLVTVNQCRQYWGARITDA 198
                                                                                                                                                                                                                                                    MICAGGSGASSCQGDSGGPLVCQKGNTWVLIGIVSWGTKNCNIQAPAMYTRVSKFSTWIN 258
                                                                                                                                                                                                                                                                   TPGRHFVVLGEYDRSSNAEPVQVLSIARAITHPNWNANTMNNDLTLLKLASPARYTAQVS 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PVCLASTNEALPSGLTCVTTGWG--RISGVGNVTPARLQQVVLPLVTVNQCRQYWGAR-I 195
                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                               1 CGVPAIQPVLSGLSRIVNGEEAVPGSWPWQVSLQDKTGFHFCGGSLINENWVVTAAHCGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19 CGVPAITPALSYNQRIVNGENAVPGSWPWQVSLQDNTGFHFCGGSLISPNWVYTAAHCQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGVPAITPALSYNQRIVNGENAVPGSWPWQVSLQDNTGFHFCGGSLISPNWVVTAAHCQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TDAMICAGGSGASSCQGDSGGPLVCQKGNTWVLIGIVSWGTKNCNIQAPAMYTRVSKFST
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(&
   Length 245;
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                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63;
   DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pancreatic elastase II (EC 3.4.21.71) precursor - pig
N;Alternate names: pancreatopeptidase E
C;Species: Sus scrofa domestica (domestic pig)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 737; DB 2;
Pred. No. 9.9e-54;
54.6%; Score 774.5; DB 1
57.3%; Pred. No. 7.9e-57;
ive 32; Mismatches 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: protein
A;Residues: 1-14;15-24 <LET>
C;Superfamily: trypsin; trypsin homology
F;15-237/Domain: trypsin homology <TRY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52.0%;
54.2%;
                                Conservative
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es 135; Conserv
                Similarity
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WVDQILAAN
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Best Local Simil
Matches 141; C
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pancreatic elastase II (EC 3.4.21.71) precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 18-laug-1982 #sequence_revision 18-laug-1982 #text_change 24-Sep-1999
C;Accession: A00961
R;MacDonald, R.J.; Swift, G.H.; Quinto, C.; Swain, W.; Pictet, R.L.; Nikovits, W.; Ru
Bjochemistry 21, 1453-1463, 1982
A;Title: Primary structure of two distinct rat pancreatic preproelastases determined
A;Reference number: A00960; MUID:82182967; PMID:6918221
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A; Residues: 1-271 <MAC>
A; Cross-references: 0B:100124; GB:J00731; NID:g204019; PIDN:AAA98780.1; PID:g204021
A; Cross-references: GB:L00124; GB:J00731; NID:g204019; PIDN:AAA98780.1; PID:g204021
C; Superfamily: trypsin; trypsin homology
C; Keywords: hydrolase; pancreas; serine proteinase; zymogen
F;1-16/Domain: activation peptide #status predicted <APT>
F;1-30/Domain: activation peptide #status predicted <APT>
F;31-271/Product: elastase II #status predicted <APT>
F;31-284/Domain: trypsin homology <TRY>
F;31-284/Domain: trypsin homology <TRY>
F;75,123,218/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                      elastase II mRNAs
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16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 22-Jun-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             119 N--NDLTLLKLASPARYTAQVSPVCLASTNEALPSGLTCVTTGWGRISGVGNVTPARLQQ 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 SNGNDIALLKLASPVSLTDKIQLGCLPAAGTILPNNYVCYVTGWGRLQTNG-ASPDILQQ 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LLLSLTLSLVLLGSSWGCGVPAITPALSYN-QRIVNGENAVPGSWPWQVSLQ---DNTGF 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         177 VVLPLVTVNQCRQ--YWGARITDAMICAGGSG-ASSCQGDSGGPLVCQKGN-TWVLIGIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16;
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41.1%; Pred. No. 1.8e-35;
Live 46; Mismatches 100;
                                               I.; Tani, T.; Shimoda, K.; Takiguchi, Y.
2, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 37.9%; Score 537; DB 2
Best Local Similarity 43.1%; Pred. No. 4e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48; Mismatches
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Best Local Similarity
Matches 113; Conserv
                                               C; Accession: A26823
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pancreatic elastase (EC 3.4.21.36) IIIB precursor - human N;Alternate names: 35K glycoprotein; pancreatic protein P35; protein G32; proteinase C;Species: Homo sapiens (man) C;Date: Homo sapiens (man) C;Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 22-Jun-1999 C;Accession: B29934; A90516; A27206; A33257; A28932; S04999; S04490 C;Accession: B29934; A90516; A27206; A33257; A28932; S04999; S04490 J:Mita, X; Mita, K; Taktguchi, Y. 3. 3. 3. 1231-1239, 1988 A;Title: Identification of a novel class of elastase isozyme, human pancreatic elasta A;Reference number: A92664; MUID:88087253; PMID:2826474
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A; Residues: 18-57 < AVI.

A; Residues: 18-57 < AVI.

Biochem. Biophys. Res. Commun. 156, 318-322, 1988

A; Title: Characterization of two glycoproteins of human pancreatic juice: P35, a trun A; Reference number: A28932: MUID: 89025862; PMID: 3178837

A; Roccession: A2893. MUID: 89025862; PMID: 3178837

A; Roccession: A2893. MUID: 89025862; PMID: 3178837

A; Molecule type: protein

A; Residues: 'X, 73-52, 'X, 54-55, 'XXX', 59-63 < GUY.

B; Moulard, M: Kerfelec, B.; Mallet, B.; Chapus, C.

FEBS Lett. 250, 166-170, 1989

A; Title: Identification of a procarboxypeptidase A-truncated protease E binary comple A; Reference number: S04999; MUID: 89325560; PMID: 2753124

A; Accession: S04999

A; Molecule type: protein

A; Residues: 31-50 < AMOU.

FEBS Lett. 249, 275-278, 1988

A; Mendorf, P.; Geyer. R.; Szlegoleit, A.; Linder, D.

FEBS Lett. 249, 275-278, 1988

A; Title: Loccalization and characterization of the glycosylation site of human pancrea

A; Reference number: S04999; MUID: 89289996; PMID: 2737288
                                                                                                                                                                                                                                              SKGNDIALLKLANPVSLTDKIQLACLPPAGTILPNNYPCYVTGWGRLQTNGAV-PDVLQQ 175
                                                                                                                                                                                                                                                                                                                                                                            59 FCGGSLISPNWVVTAAHCQVTPGRHFVVLGEYDRSSNAEPVQVLSIARAITHPNWNANTM 118
                                                                                                                                     57 TCGGSLIANSWVLTAAHCISSSRTYRVGLGRHNLYVAESGSLAVSVSKIVVHKDWNSNQI 116
                                                                                                                                                                                                       N--NDLTLLKLASPARYTAQVSPVCLASTNEALPSGLTCVTTGWGRISGVGNVTPARLQQ 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-270 <TAN>
A;Cross-references: GB:M18692; NID:g607029; PIDN:AAA58454.1; PID:g182035
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A;Molcoule type: mRNA
A;Residues: 'G',5-63,'G',65-78,'W',80-118,'G',120-163,'P',165-270 <SHE>
R;Fletcher, T.S.
       MIRTLLLSTLVAG-ALSCGDPTYPP---YVTRVVGGEEARPNSWPWQVSLQYSSNGKWYH
                                                                                                                                                                                                                                                                                                                                            VVLPLVTVNQCRQ - - YWGARITDAMICAGGSGA - SSCQGDSGGPLVCQKGN - TWVLIGIV
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Blochemistry 26, 3447-3452, 1987
A;Title: Primary structure of human pancreatic protease
A;Reference number: A90516; MUID:88000545; PMID:3477287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWGTK-NCN-IQAPAMYTRVSKFSTWINQVMAYN 264
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A; Accession: A27206
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A; Reference number: A94507
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A;Molecule type: mRNA
A;Residues: 1-269 cKAM>
A;Residues: 1-269 cKAM>
A;Cross-references: CB:MI6652; NID:g182057; PIDN:AAA52380.1; PID:g182058
B;Fletcher, T.S.; Shen, W.F.; Largman, C.
Biochemistry 26, 7256-7261, 1987
A;Title: Primary structure of human pancreatic elastase 2 determined by sequence analysi
A;Reference number: A27432; MUID:88107669; PMID:3427074
A;Accession: A27432
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R;Shirasu, Y.; Yoshida, H.; Matsuki, S.; Takemura, K.; Ikeda, N.; Shimada, Y.; Ozawa, T.
Bicchem. 102, 1555-1563, 1997
A;Title: Molecular cloning and expression in Escherichia coli of a cDNA encoding human
A;Reference number: A41431; MUID:88198076; PMID:2834346
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                                                                                                                                                                                                                                                                      231
   HFCGGSLISPNWVVTAAHCQVTPGRHFVVLGEYDRSSNAEPVQVLSIARAITHPNWNANT 117
                                                               HTCGGSLVANNWVLTAAHCISNSRTYRVLLGRHSLSTSESGSLAVQVSKLVVHEKWNAQK 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PID:9219620
as Cys
                                                                                                                                                                        MN--NDLTLLKLASPARYTAQVSPVCLASTNEALPSGLTCVTTGWGRISGVGNVTPARLO
                                                                                                                                                                                                                                                                   QVVLPLVTVNQC -- RQYWGARITDAMICAGGSG-ASSCQGDSGGPLVCQKGN-TWVLIGI
                                                                                                                                                                                                                                                                                                                                  QGRLLVVDYATCSSASWWGSSVKTNMVCAGGDGVTSSCNGDSGGPLNCQASNGQWQVHGI
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C.Superfamily: trypsin; trypsin homology
C.Superfamily: trypsin; trypsin homology
C.Superfamily: trypsin; trypsin properties
F.1-16/Domain: signal sequence status predicted <SIG>
F.17-28/Domain: propeptide *status predicted <PRO>
F.29-269/Product: pancreatic elastase IIA *status predicted <MAT>
F.29-262/Domain: trypsin homology <TRY>
F.31-21,216/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36.3%; Score 515; DB 2; Length 26 llarity 41.6%; Pred. No. 2.7e-35; Conservative 47; Mismatches 97; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A, Accession: A41431
A, Molcoule type: mRNA
A, Residues: 1-201, V, 203-269 (SHI>
A, Cross-references: GB:D00236; NID:g219619; PIDN:BAA00165.1;
A, Note: the authors translated the codon GTG for residue 202
R:Moulard, M.: Michon, T.; Kerfelec, B.; Chapus, C.
FEBS Lett. 261, 179-183, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Title: Further studies on the human pancreatic binary Reference number: 808253; MUID:90169111; PMID:2307232
                                                                                                                                                                                                                                                                                                                                                                                                    VSWG-TKNCNI-QAPAMYTRVSKFSTWINQVMAYN 264
                                                                                                                                                                                                                                                                                                                                                                                                                                           Cross-references: GDB:119866; OMIM:130120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;Molecule type: protein
;Residues: 'X',18-50 <MOU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Molecule type: mRNA
Residues: 1-269 <FLE>
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C;Accession: $68825
R;Tomomura, A.; Akiyama, M.; Itoh, H.; Yoshino, I.; Tomomura, M.; Nishii, Y.; Noikura
FEBS Lett. 386, 26-28, 1996
                                                                                                                                                                                                                                                                                                                  C;Accession: S68826
R;Tomonura, A.; Akiyama, M.; Itoh, H.; Yoshino, I.; Tomonura, M.; Nishii, Y.; Noikura FEBS Lett. 386, 26-28, 1996
A;Title: Molecular cloning and expression of human caldecrin.
A;Reference number: S68825; MUID:96221265; PMID:8635596
A;Accession: S68826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pancreatic elastase (EC 3.4.21.36) isoform 1 precursor - human
NiAlternate names: caldecrin isoform 1
C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Date: 04-Dec-1997 #sequence_revision 12-Dec-1997 #text_change 28-May-1999
                                                                                                                                                                                                        pancreatic elastase (EC 3.4.21.36) isoform 2 precursor - human NiAlternate names: caldecrin isoform 2 C. Species: Homo sapiens (man) C. Species: Homo sapiens (man) C. Species: Homo sapiens (pan) Resquence_revision 12-Dec-1997 #text_change 30-Jan-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:S82198; NID:91839466; PIDN:AAB47104.1; PID:91839467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NNDLTLLKLASPARYTAQVSPVCLASTNEALPSGLTCVTTGWGRISGVGNVTPARLQQVV 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGGSLISPNWVVTAAHCQVTPGRHFVVLGEYD-RSSNAEPVQVLSIARAITHPNWNANTM 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59 CGGTLIASNFVLTAAHCISNTWTYRVAVGKNNLEVEDEEGSLFVGVDTIHVHKRWNALLL 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   119 RNDIALIKLAEHVELSDTIQVACLPEKDSLLPKDYPCYVTGWGRLWTNGPIAD-KLQQGL 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               179 LPLVTVNQCRQ--YWGARITDAMICAGGSGA-SSCQGDSGGPLVCQKGN-TWVLIGIVSW 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 LLSLTLSLVLLGSSWGCGVPAITPALSYNQRIVNGENAVPGSWPWQVSLQ---DNTGFHF 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-268 < TOM>
A; Residues: 1-268 < TOM>
C; Superfamily: trypsin; trypsin homology
C; Keywords: hydrolase; pancreas; serine proteinase; zymogen
F; 1-16/Domain: signal sequence #status predicted < SIG>
F; 1-29/Domain: propeptide #status predicted < PRO>
F; 30-268/Product: pancreatic alastase isoform 2 #status predicted < MAT>
F; 30-262/Domain: trypsin homology < TRX>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A. Experimental source: pancreas
C. Superfamily: trypsin; trypsin homology
C. Keywords: hydrolase; pancreas; serine proteinase; zymogen
F. 1-16. Domain: signal sequence #status predicted <SIG>
F:17-29. Domain: propeptide #status predicted <PRO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34.9%; Score 495.5; DB 2;
40.1%; Pred. No. 1.1e-33;
Live 46; Mismatches 102;
                               ||||: |:::||::|| | ||:|| |
1494 SWGSGKCDVKAPSVYTLTSAFMDWISQHM 1522
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   SWGTKNCNIQAPAMYTRVSKFSTWINQVM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 108; Conserv
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A; Residues: 1-268 <TOM>
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   233
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R; Yang, J.C.; Lindsay, L.L.; Hedrick, J.L.
submitted to the EMBL Data Library, March 1998
A; Description: cDNA cloning of ovochymase, a chymotrypsin-like protease released from Xe
                                                                                                                                                                                                                                                                                                                                                                                                                            10;
A Residues: 94-128;132-164 < WEN>
A; Residues: 94-128;132-164 < WEN>
C; Superfamily: trypsin, trypsin homology
C; Superfamily: trypsin, trypsin homology
C; Keywords: glycoprotein; hydrolase; serine proteinase; zymogen
E;1-17/Domain: scipnal sequence #status predicted <ACT>
F;18-28/Domain: activation peptide #status predicted <ACT>
F;29-270/Product: (or 31-270) pancreatic elastase IIIB #status predicted
F;29-563/Domain: trypsin homology <TRX>
F;29-573/Active site: His, Asp, Ser #status predicted
F;14/Rainding site: carbohydrate (Asn) (covalent) #status experimental
F;153/Binding site: carbohydrate (Asn) (covalent) #status absent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polyprotein - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1382 DLLLLELDTPLLLNNSVAVIC-----LPDDVTTDWTQAECLVAGWG-VTDVGGMSLPT 1433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1264 CGNTTVDPMMLYMARSGKIRNLNKGGKESGRVVGGQQAAPRSWPWLVSIQNSKKRHYCGG 1323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-1524 </AN>
A;Cross-references: EMBL:U81290; NID:g2981640; PID:g2981641; PIDN:AAC24717
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DLTLLKLASPARYTAQVSPVCLASTNEALPSGLT-----CVTTGWGRISGVGNVT-PA 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RLQQVVLPLVTVNQCRQYWGARITDAMICAGGSGASSCQGDSGGPLVCQKGNTWVLIGIV 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59 FCGGSLISPNWVVTAAHCQVTPGRHFVVLGEYDRSSNAEPVQVLSI--ARAITHPNWNAN 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            117 TM--NNDLTLLKLASPARYTAQVSPVCLASTNEALPSGLTCVTTGWGRISGVGNVTPARL 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 176 QEALLPVVDYEHCSRWNWWGSSVKKTMVCAGGDIRSGCNGDSGGPLNCPTEDGGWQVHGV 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LLLSLTLSLVLLGSSWGCGVPAITPALSYNQRIVNGENAVPGSWPWQVSLQ-DNTG--FH 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MMLRILSSLILVAVASGYGPPSSRP----SSRVVNGEDAVPYSWPWQVSLQYEKSGSFYH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QQVVLPLVTVNQCRQ -- YWGARITDAMICAGGSGASSCQGDSGGPLVC-QKGNTWVLIGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57 TCGGSLIAPDWVVTAGHCISSSRTYQVVLGEYDRAVKEGPEQVIPINSGDLFVHPLWNRS
                                                                                                                                                                                                                                                                                                                                                                                                                            17;
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                                                                                                                                                                                                                                                                                                                                                                    Length 270;
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                                                                                                                                                                                                                                                                                                                                                                 ; Score 513.5; DB 2; Length 2; Pred. No. 3.5e-35; 46; Mismatches 97; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |: :| || : :|||| || : :|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         232 VSW-GTKNCNI-QAPAMYTRVSKFSTWINQVMA 262
                                                                                                                                                                                                                                                                                                                                                                    36.2%;
                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 41.49
Matches 113; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Reference number: Z20829
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                                                                                                                   119 NNDLTLLKLASPARYTAQVSPVCLASTNEALPSGLTCVTTGWGRISGVGNVTPARLQQVV 178
                                                                                                                                                                                                       Query Match 34.9%; Score 495.5; DB 2; Length 268; 'Best Local Similarity 40.1%; Pred. No. 1.1e-33; Matches 108; Conservative 46; Mismatches 102; Indels 13; Gaps
                                                                       F;30\text{-}268/Product: pancreatic elastase isoform 1 #status predicted <MAT> F;30\text{-}262/Domain: Lrypsin homology <TRY>
                                                                                                                                                                                                                                                235 GT-KNCNI-QAPAMYTRVSKFSTWINOVM 261
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Search completed: December 20, 2002, 15:19:48 Job time : 17.6957 secs

No. of

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Gencore version 5.1.3

Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 20, 2002, 15:14:28 ; Search time 14.6087 Seconds

(without alignments)
1520.126 Million cell updates/sec
Title:
Perfect score: 1221
Sequence: 121
Sequence: 121LLLSLTLSLVLLGSSWGCG.......GDSGGPLVCQKGNTWVLIGI 231
Scoring table: BLOSUW62
Gapop 10.0 , Gapext 0.5
Searched: 283224 seqs, 96134422 residues
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	chymotrypsin-like	chymotrypsin (EC 3	chymotrypsin (EC 3	chymotrypsin (EC 3	chymotrypsin (EC 3				pancreatic elastas	pancreatic elastas	chymotrypsin-like	pancreatic elastas	<u>ස</u>	polyprotein - Afri			plasmin (EC 3.4.21	enteropeptidase (E	plasmin (EC 3.4.21	pancreatic elastas	pancreatic elastas	procarboxypeptidas	plasmin (EC 3.4.21	plasmin (EC 3.4.21	mast cell tryptase				
SUMMARIES	QI	813	A21195	S47537	A31299	KYRTB	KYBOB	KYBOA	S72219	A26823	B29934	A23473	B26823	ELRT2	C26823	A29934	A25528	A57014	T30337	B61545	PLHU	B30848	A43090	PLPG	S68826	568825	CPBOA3	PLMS	A61545	S56160
	80	7	7	7	~	٦	Н	-	7	~	7	~	~	Н	7	~	~	Н	7	~	Н	7	-	Н	~	7	Н	Н	7	7
	Length	264	263	263	263	263	245	245	244	269	270	126	269	271	269	270	271	343	1524	460	810	810	1035	790	268	268	240	812	455	270
a	Match	99.4	58.5	57.5		54.9			53.5	38.7		36.9		35.9	35.0	34.4				33.1	32.5	32.4					31.9			
	Score	1214	714.5	701.5	689.5	670.5	666.5	657.5	653	472	453.5	451	445	438	427	420.5	415	410.5	409	404	397	396	395.5	~		390.5		389.5	œ	œ
Poent	NON	1	7	m	4	S.	φ	7	60	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

RESULT 2
A21195
chymotrypsin (EC 3.4.21.1) 2 precursor - dog
c.)Species: Canis lupus familiaris (dog)
C.)Bate: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 22-Jun-1999
C.)Accession: A21195

serine proteinease	Oviductin (EC 3.4. trypsin (EC 3.4.21	trypsin (EC 3.4.21	tryptase (EC 3.4.2	trypsin (EC 3.4.21	trypsin (EC 3.4.21	enteropeptidase (E	trypsin (EC 3.4.21	plasma kallikrein	plasmin (EC 3.4.21	low-density lipopr	trypsin (EC 3.4.21	pancreatic elastas	pancreatic elastas	trypsin (EC 3.4.21
A47547	T30338 S55067	S31779	A47246	TRRT1	TRDGC	A56318	S55066	KQHUP	PLBO	JE0315	TRPGTR	JQ1473	ELRT1	TRDG
<b>~</b> (	7 (7	7	7	٦	-	7	7	Н	П	~	Н	7	Н	┥,
786	248	238	273	246	246	1019	248	638	812	1113	231	268	266	247
31.6	31.5	31.5	31.5	31.4	31.4	31.3	31.0	31.0	30.9	30.9	30.9	30.8	30.8	30.8
386	386 385	384.5	384.5	383.5	383.5	382	379	378.5	377.5	377.5	377	376.5	376	375.5
30	37 32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

283224

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_73:*
: pir1:*
: pir2:*
: pir3:*

Database :

RESULT 1 138136 Chyotrypsin-like proteinase (EC 3.4.21) CTRL-1 - human Chymotrypsin-like proteinase (EC 3.4.21) CTRL-1 - human C; Species: Homo sapiens (man) C; Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 22-Jun-1999 C; Accession: 138136 E; Accession: 138136 E; Aristensen, F.; Solhelm, J.; Kristensen, T.; Kolsto, A.B.; Prydz, H. Hum. Mol. Genet. 2, 1589-1595, 1993 A; Title: A tight cluster of five unrelated human genes on chromosome 16q22.1. A; Recence number: 138135; MuID: 94093544; PMID: 8268911 A; Accession: 138136 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: DNA A; Residues: 1-264 ARES A; Cross-references: EMBL: X71874; NID: 9406226; PIDN: CAA50710.1; PID: 9406228 A; Cross-references: GDB: 204061 A; Cross-references: GDB: 204061 A; Cross-references: GDB: 204061 A; Introns: 18/1; 52/2; 79/2; 106/3; 167/1; 211/3 C; Superfamily: trypsin; trypsin homology C; Superfamily: trypsin homology A; TRX> E; 34.257/Domain: trypsin homology A; 287, 281, 281, 281, 281, 281, 281, 281, 281
Query Match 99.4%; Score 1214; DB 2; Length 264; Best Local Similarity 99.6%; Pred. No. 3.2e-95; Matches 230; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
MLLLSLTLSLVLLGSSWGCGIPAIKPALSFSQRIVNGENAVLGSWPWQVSLQDSSGFHFC
Oy 61 GGSLISOSWVVTAAHCNVSPGRHFVVLGEYDRSSNAEPLQVLSVSRAITHPSWNSTTMNN 120
QY 121 DVTLKLASPAQYTTRISPVCLASSNBALTEGLICVTGWGRLSGVGNVTPAHLQQVALP 180
Qy 181 LVTVNQCRQYWDSSITDSMICAGGAGASSCQGDSGGPLVCQKGNTWVLIGI 231 

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R;Pinsky, S.D.; LaForge, K.S.; Luc, V.; Scheele, G.
Proc. Natl.: Acad. Sci. U.S.A. 80, 7486-7480, 1983
A;Title: Identification of CDNA clones encoding secretory isoenzyme forms: sequence A;Reference number: A21195, WUID:84170253; PMID:6584866
                                                                                                                                                                                                                                                                                                                                                                                                                                      ï
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chymotrypsin (EC 3.4.21.1) precursor - Atlantic cod
C;Species: Gadus morhua (Atlantic cod)
C;Date: 26-Dec-1994 Hesquence_revision 03-Aug-1995 #text_change 22-Jun-1999
C;Accession: S47537; S43163
R;Gudmundsdottir, A.; Oskarsson, S.; Eakin, A.E.; Craik, C.S.; Bjarnason, J.B.
Biochim. Biophys. Acta 1219, 211-214; 1994
A;Title: Atlantic cod cDNA encoding a psychrophilic chymotrypsinogen.
A;Reference number: S47537; MUID:94368860; PMID:8086467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGSLISQSWVVTAAHCNVSPGRHFVVLGEYDRSSNAEPLQVLSVSRAITHPSWNSTTMNN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DVTLLKLASPAQYTTRISPVCLASSNEALTEGLTCVTTGWGRLSGVGNVTPAHLQQVALP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72 TAAHCNVK-NYHRVVLGEHDRSSNSEGVQVMTVGQVFKHPRYNGFTINNDILLVKLATPA 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PID:9468751
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            132 QYTTRISPVCLASSNEALTEGLTCVTTGWGRLSGVGNVTPAHLQQVALPLVTVNQCRQYW 191
                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12 LLGSSWGCGIPAIKPALSFSQRIVNGENAVLGSWPWQVSLQDSSGFHFCGGSLISQSWVV 71
                                                                                                                                                                                                                     PID:9163946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MAPLWLLSCFALLGTAFGCGVPALQPVLSGLSRIVNGEDAVPGSWPWQVSLQDSTGFHFC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MLLLSLTLSLVLLGSSWGCGIPAIKPALSFSQRIVNGENAVLGSWPWQVSLQDSSGFHFC
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                                                                                                                                                                                                                                                                                                                                                                              Score 714.5; DB 2; Length 263;
Pred. No. 5e-53;
5; Mismatches 64; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 57.5%; Score 701.5; DB 2; Length 263; Best Local Similarity 58.6%; Pred. No. 6.3e-52; Matches 129; Conservative 33; Mismatches 57; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LVTVNQCRQYWDSSITDSMICAGGAGASSCQGDSGGPLVCQKGNTWVLIGI 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:X78490; NID:9468750; PIDN:CAA55242.1;
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; protein digestion; serine proteinase
                                                                                                                                                                                                          A, Cross-references: GB:K01173; NID:g163945; PIDN:AAA30841.1; C:Superfamily: trypsin; trypsin homology C:Keywords: hydrolase, protein digestion; serine proteinase F:34-256/Domain: trypsin homology C:Keywords: trypsin homology CF:75,120,213/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;75,120,213/Active site: His, Asp, Ser #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                      35; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                 58.5%; Score 714.5; 56.7%; Pred. No. 5e-
                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 56.79
1; Conservative
                                                                                                                                  A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-263 <PIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-263 <GUD>
                                                                                                               A; Accession: A21195
                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 131;
                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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Biochem, Biophys. Res. Commun. 158, 569-575, 1989
A;Title: Molecular cloning and nuclectide sequence of human pancreatic prechymotryps: A;Reference number: A31299; MUID:89134264; PMID:2917002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Bell, G.I.; Quinto, C.; Quiroga, M.; Valenzuela, P.; Craik, C.S.; Rutter, W.J. J. Biol. Chem. 259, 14265-14270, 1984
A;Title: Isolation and sequence of a rat chymotrypsin B gene.
A;Reference number: A22658; MUID:85054881; PMID:6209274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chymotrypsin (EC 3.4.21.1) precursor - human
C;Species: Homo sapiens (man)
C;Date: 08-Jun-1989 #sequence_revision 08-Jun-1989 #text_change 22-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 GGSLISQSWVVTAAHCNVSPGRHFVVLGEYDRSSNAEPLQVLSVSRAITHPSWNSTTMNN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                     A Molecule type: mRNA
A; Residues: 1-263 <TOM>
A; Residues: 1-263 <TOM>
A; Cross-references: GB:MZ4400; NID:g181189; PIDN:AAA52128.1; PID:g181190
C; Genetics:
A; Gene: GDB:CTRB1; CTRB
A; Cross-references: GDB:119820; OMIM:118890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references: GB: K02298; NID: 9203653; PIDN: AAA98732.1; PID: 9203654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MAFLWLLSCWALLGTTFGCGVPAIHPVLSGLSRIVNGEDAVPGSWPWQVSLQDKTGFHFC
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C; Reywords: hydrolase; panceras; protein digestion; serine
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-33/Domain: propeptide #status predicted <PRO>
F:34-25/Product: Ghymotrypsin B #status predicted <MAT>
F:34-25/Domain: trypsin homology <TRY>
F:75,120,213/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Map position: 16q23.1-16q23.1
C; Superfamily: trypsin: trypsin homology
C; Reywords: hydrolase; protein digestion; serine proteinas
F; 34.256/Domain: trypsin homology <TRY>
F; 75,120,213/Active site: His, Asp, Ser #status predicted
67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56.5%; Score 689.5; DB 255.4%; Pred. No. 6.5e-51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Sim:
Matches 128;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121
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A; Molecule type: protein
A; Residues: 1-101, /N./103-245 < MBL>
A; Residues: 1-101, /N./103-245 < MBL>
A; Residues: 1-101, /N./103-245 < MBL>
A; Note: disulfide bonds were determined
B; Cutruzzola, F.; Ascenzi, P.; Barra, D.; Bolognesi, M.; Menegatti, E.; Sarti, P.; Sc
Biochim. Biophys. Acta 1161, 201-208, 1993
A; Title: Selective oxidation of Met-192 in bovine alpha-chymotrypsin. Effect on catal
A; Reference number: S29650; MUID:93160238; PMID:8431470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Rocelle type: protein
A; Residues: 1-12;16-27;149-160;181-200 <CUT>
A; Rolecule type: protein
A; Residues: 1-12;16-27;149-160;181-200 <CUT>
R; Smillie, L.B.; Hartley, Bs.
B; Smillie, L.B.; Hartley, Bs.
B; Smillie, L.B.; Hartley, Bs.
A; Reference number: A90236; MUD:67181723; PMID:5971785
A; Contents: annotation; active site
R; Birktoft, J.J.; Blow, D.M.; Henderson, R.; Steitz, T.A.
A; Contents: annotation; Aray crystallography
A; Title: The structure of alpha-chymotrypsin.
A; Reference number: A93754
A; Contents: annotation; X-ray crystallography
C; Comment: Tryptic cleavage after Arg-15 results in a fully active enzyme (pi-chymotrypsin; further chymotryptic cleavage liberates the dipeptide Thr-147 and Asn-148 directly from chymotryptic cleavage liberates the dipeptide Thr-147 and Asn-148 directly from chymotryptic protein digestion; serine proteinase; zymogen C; Superfamily: trypsin; trypsin homology
C; Superfamily: trypsin homology after experimental <2VM>
F; 1-45/Product: chymotrypsinogen #status experimental <2VM>
F; 1-24,0-24,0-28,136-201,168-182,191-220/Disulfide bonds: #status experimental
F; 57,102,195/Active site: His, Asp, Ser #status experimental
                                                                                                                                                        diagonal paper electrophoresis. The disu-p PMID:5971783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vanacek, J.; Keil, B.; S
                                                                                                                                                                                                                                                                                                A; Molecule type: protein
A; Residues: 1-101, N', 103-245 <BRO>
A; Residues: 1-101, N', 103-245 <BRO>
A; Residues: 1-101, N', 103-245 <BRO>
Nature 221, 337-340, 1969
A; Title: Role of a buried acid group in the mechanism of action of chymotrypsin.
A; Reference number: A331-8; MulD: 69106266; PMID: 5764436
A; Contents: annotation; revision to readed 102
B; Meloun, B.; Kluh, I.; Kostka, V.; Moravek, L.; Prusik, Z.; Vanacek, J.; Keil, Biochim. Biophys. Acta 130, 543-546, 1966
A; Title: Covalent structure of bovine chymotrypsinogen A.
A; Reference number: A90572; MulD: 67183948; PMID: 5972866
A; Accession: A93158
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Accession: A90235; A93158; S29650; A00952
                                           R;Brown, J.R.; Hartley, B.S.
Biochem. J. 101, 214-228, 1966
A;Title: Location of disulphide bridges by
A;Reference number: A90235; MUID:67181721;
A;Accession: A90235
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N.Alernate names: chymotrypsinogen B
C; Species: Bos primigenius taurus (cattle)
C; Date: 08-Oct-1981 #sequence_revision 08-Oct-1981 #text_change 18-Jul-1997
C; Accession: A00953
R; Smillie, L.B.; Furka, A.; Nagabhushan, N.; Stevenson, K.J.; Parkes, C.O.
Nature 218, 343-346, 1968
A; Title: Structure of chymotrypsinogen B compared with chymotrypsinogen A and trypsinoge
A; Recence number: A00953; MUD: 68238908; PMID: 5649671
A; Recence number: A00953
A; Molecule type: protein
A; Recession: A00953
A; Molecule type: protein
A; Recession: A00953
C; Comment: The first activation cleavage, leading to pi-chymotrypsinogen A, in the acin C; Comment: The first activation cleavage, leading to pi-chymotrypsin B, occurs in the saft C; Superfamily: trypsin homology
C; Superfamily: trypsin perpeptide #status experimental <AMAT>
F; 1-15/Domain: propeptide #status experimental <AMAT>
F; 1-245/Froduct: chymotrypsin B #status experimental <AMAT>
F; 1-223/Domain: trypsin homology <ATRY>
F; 1-122, 42-58, 136-201, 168-182, 191-220/Disulfide bonds: #status experimental
F; 57, 102, 195/Active site: His, Asp, Ser #status experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          139 PVCLASSNEALTEGLITCVTTGWGRLSGVGNVTPAHLQQVALPLVTVNQCRQYWDSSITDS 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 DVTLLKLASPAQYTTRISPVCLASSNEALTEGLTCVTTGWGRLSGVGNVTPAHLQQVALP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79 SPGRHFVVLGEYDRSSNAEPLQVLSVSRAITHPSWNSTTMNNDVTLLKLASPAQYTTRIS 138
                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                 Length 263,
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                                      54.9%; Score 670.5; DB 1;
53.2%; Pred. No. 2.6e-49;
1ve 35; Mismatches 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62;
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Best Local Similarity 57.3%; Pred. No. 5.2e-49;
Matches 122; Conservative 28; Mismatches 62
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Matches 123; Conservative
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117 SNGNDIALLKLASPVSLTDKIQLGCLPAAGTILPNNYVCYVTGWGRLQTNG-ASPDILQQ 175
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A;Reference number: A90958; MUID:87217962; PMID:3646943
                                                                                                                                                                         Ricth-Larsen, R.; Asgeirsson, B.; Thorolfsson, M.; Norregaard-Madsen, M.; Hojrup, P. Biochim. Biophys. Acta 1297, 49-56, 1996
A;Title: Structure of chymotrypsin variant B from Atlantic cod, Gadus morhua.
A;Reference number: S72219; MUID:96439045; PMID:8841380
A;Accession: S72219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
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chymotrypsin B - Atlantic cod (fragments)
C;Species: Gadus morhua (Atlantic cod)
C;Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 07-Aug-1998
C;Accession: S72219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pancreatic elastase II (EC 3.4.21.71) precursor - pig
N'Alternate names: pancreatopeptidase E
C.Species: Sus scrofa domestica (domestic pig)
C.Date: 16-Aug-1988 #sequence_revision.16-Aug-1988 #text_change.22-Jun-1999
C.Accession: A.268.3
R.Kawashima, I.; Tani, T.; Shimoda, K.; Takiguchi, Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 RT-YHRVIVGEHDKASD-ENIQILKPSMVFTHPKWDSRTINNDISLIKLASPAVLGTNVS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119 N--NDVTLLKLASPAQYTTRISPVCLASSNEALTEGLTCVTTGWGRLSGVGNVTPAHLQQ 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       139 PVCLASSNEALTEGLTCVTTGWG--RLSGVGNVTPAHLQQVALPLVTVNQCRQYW-DSSI 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59 FCGGSLISQSWVVTAAHCNVSPGRHFVVLGEYDRSSNAEPLQVLSVSRAITHPSWNSTTM 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19 CGIPAIKPALSFSQRIVNGENAVLGSWPWQVSLQDSSGFHFCGGSLISQSWVVTAAHCNV 78
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A; Molecule type: mRNA
A; Molecule type: mln
A; Molecule t
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. 1.6e-32;
rrhes 84; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 244;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                196 TDSMICAGGAGASSCQGDSGGPLVCQKGNTWVLIGI 231
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                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-14;15-244 <LET>
C;Superfamily: trypsin; trypsin homology
F;15-237/Domain: trypsin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 57.99
Matches 125; Conservative
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A; Accession: A7226

A; Molecule type: DNA

A; Residues: (G, 5-63, 46, 65-78, 'W', 80-163, 'P', 165-270 <FLE>

A; Recession: A7226

A; Residues: (G, 5-63, 46, 65-78, 'W', 80-163, 'P', 165-270 <FLE>

B; Atiles, F.X.; Pascual, R.: Salva, M.; Bonicel, J.; Puigserver, A.

Biochem. Biophys. Res. Commun. 163, 1191-1196, 1989

A; Reference number: A33257; MUID:89392022; PMID:2675835

A; Accession: A33257

A; Molecule type: protein

A; Residues: 18-57 <AVI>

B; Molecule type: protein

A; Reference number: A28932; MUID:89025862; PMID:3178837

A; Accession: A28932

A; Molecule type: protein

A; Reference number: A28932; MUID:89025862; PMID:3178837

A; Accession: A28932

A; Molard, M.; Kerfelec, B.; Mallet, B.; Chapus, C.

R; Moulard, M.; Kerfelec, B.; Mallet, B.; Chapus, C.

R; Moulard, M.; Rerfelec, B.; Mullet, B.; Chapus, C.

R; Moulard, M.; Rerfelec, B.; Mullet, B.; Chapus, C.

A; Title: Identification of a procarboxypeptidase A-truncated protease E binary comple A; Reference number: S04999; MUID:89325560; PMID:2753124
                                                                                                                                                                                                                                        pancreatic elastase (EC 3.4.21.36) IIIB precursor - human
N.Alternate names: 35K glycoprotein; pancreatic protein P35; protein G32; proteinase
C; Species: Homo sapiens (man)
C;Dec.1988 #text_change 22-Jun-1999
C;Dec.1988 #text_change 22-Jun-1999
C;Accession: B29934; A90516; A22206; A33257; A28932; S04999; S04490
R;Tani, T.; Ohsumi, J.; Mita, K.; Takiguchi, Y.
J. Biol. Chem. 263, 1231-1239, 1988
A;Title: Identification of a novel class of elastase isozyme, human pancreatic elasta
A;Reference number: A22664; MUID:88087253; PMID:2826474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     predicted <MAT>
                               A; Molecule type: mRNA
A; Residues: 'G',5-63, 'G',65-78,'W',80-118,'G',120-163,'P',165-270 <SHE>
R; Fletcher, T.S.
Submitted to GenBank, August 1987
A; Reference number: A94507
A; Contents: revision to residue 119
177 VALPLVTVNQCRQ--YWDSSITDSMICAGGAG-ASSCQGDSGGPLVCQKGN-TWVLIGI
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A, Residues: 94-128:132-164 
A, Residues: 94-128:132-164 
A, Residues: 94-128:132-164 
A, Residues: 94-128:132-164 
C, Superfamily: trypsin; trypsin homology
C, Superfamily: trypsin; trypsin homology
C, Reywords: glycoprotein: hydrolase; serine proteinase; zymogen
E; 1-17/Domain: stronalsequence #status predicted <arc>
F: 18-28/Domain: activation peptide #status predicted <arc>
F: 29-27/O/Product: (or 31-270) panoreatic elastase IIIB #status pr.
F: 29-363/Domain: trypsin homology <TRY>
F: 33-123/217/Active site: His, Asp, Ser #status predicted
F: 114/Ahinding site: carbohydrate (Asn) (covalent) #status absent
F: 153/Binding site: carbohydrate (Asn) (covalent) #status absent
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A; Residues: 31-50 CMOU>
R; Wendorf, P.; Geyer, R.; Sziegoleit, A.; Linder,
FEBS Lett. 249, 275-278, 1989
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Fri

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A; Molecule type: mRNA
A; Residues: 1-269 <FFLE>
A; Residues: 1-269 <FFLE>
A; Cross-references: GB:M16631; NID:g182022; PIDN:AAA52374.1; PID:g182023
A; Cross-references: GB:M16631; NID:g182022; PIDN:AAA52374.1; PID:g182023
B; Shirasu, Y:; Yoshida, H.; Matsuki, S.; Takemura, K.; Ikeda, N.; Shimada, Y.; Ozawa, J. Blochem. 102, 1555-1563, 1987
A; Title: Molecular cloning and expression in Escherichia coli of a cDNA encoding huma A; Reference number: A41431; MUID:88198076; PMID:2834346
                                                                          A; III. E: Primary structure of human pancreatic elastase 2 determined by sequence anal A; Reference number: A27432; MUID:88107669; PMID:3427074
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R; MacDonald, R.J.; Swift, G.H.; Quinto, C.; Swain, W.; Pictet, R.L.; Nikovits, W.; Ru
Biochemistry 21, 1453-1463, 1982
A; Title: Primary structure of two distinct rat pancreatic preproelastases determined
A; Reference number: A00960; MUID: 82182967; PMID: 6918221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-271 <MAC>
A; Cross-references: 0B:L00124; GB:J00731; NID:g204019; PIDN:AAA98780.1; PID:g204021
C; Superfamily: trypsin; trypsin homology
C; Keywords: hydrolase; pancreas; serine proteinase; zymogen
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 18-Aug-1982 #sequence_revision 18-Aug-1982 #text_change 24-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59 FCGGSLISQSWVVTAAHCNVSPGRHFVVLGEYDRSSNAEPLQVLSVSRAITHPSWNSTTM 118
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A; Residues: 1-201,'V', 203-269 <SHI>
A; Cross-references: GB:D00236; NID:g219619; PIDN:BAA00165.1; PID:g219620
A; Note: the authors translated the codon GTG for residue 202 as Gys
R; Moulard, M.; Michon, T.; Kerfelec, B.; Chapus, C.
REBS Lett. 261, 179-183, 1990
A; Title: Further studies on the human pancreatic binary complexes involvi
A; Reference number: S08253; MUID:90169111; PMID:2307232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A Map position: I2pter-12qter
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; anonceas; serine proteinase
F;1-16/Pomain: signal sequence #status predicted <SIG>F;1-7-28/Domain: propeptide #status predicted <PRO>F;29-569/Product: pancreatic elastase IIA #status predicted
F;29-262/Domain: trypsin homology <TRY>F;39-262/Domain: trypsin homology <TRY>F;31-121,216/Active site: His, Asp, Ser #status predicted
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R;Fletcher, T.S.; Shen, W.F.; Largman, Blochemistry 26, 7256-7261, 1987
A;Title: Primary structure of human par
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A;Residues: 'X',18-50 <MOU>
C;Genetics:
A;Gene: GDB:ELA1
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C;Species: Homo sapiens (man)
C;Date: 16-Aug-1988 #sequenc_erevision 16-Aug-1988 #text_change 20-Jun-2000
C;Accession: B26823; A27432; A41431; S34491
R;Kawashima, I.; Tani, T.; Shimoda, K.; Takiguchi, Y.
DNA 6, 163-172, 1987
A;Title: Characterization of pancreatic elastase II cDNAs: two elastase II mRNAs are A;Reference number: A90958; MUID:87217962; PMID:3646943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Attantive proteinase (EC 3.4.21..) - pig (tentative sequence) (fragments)
N:Alternate names: pancreatic elastase II [misidentification]
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 31-Mar-2000
C:Accession: A23473
R:Vered, M.: Gertler, A.; Burstein, Y.
Int. J. Pept. Protein Res. 27, 183-190, 1986
A:Reference number: A23473; MUID:86194934; PMID:3634756
A:Accession: A23473
A;Molcoule type: Protein
A:Residues: 1-126 <VERP
C:Superfamily: trypsin; trypsin homology
C:Keywords: hydrolase; serine proteinase
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A;Residues: 1-269 <KAM>
A;Cross-references: GB:M16652; NID:g182057; PIDN:AAA52380.1; PID:g182058
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                                             Length 270;
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Pred. No. 3.9e-31;
                                     37.1%; Score 453.5; DB 2
42.5%; Pred. No. 5.8e-31;
ilve 36; Mismatches 87
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43.7%;
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Matches 93; Conserv
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                                         Query Match
Best Local S
Matches 102
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pancreatic elastase (EC 3.4.21.36) IIIA precursor · human
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A; Molecule type: DNA
A; Residues: 1-270 <TAN>
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A;Reference number: A90958; MUID:87217962; PMID:3646943
A;Accession: C26823
                                                                                                                                                                                                                                       9.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pancreatic elastase II (EC 3.4.21.71) B precursor - human
N'Alternate names: pancreatopeptidase E
C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 22-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                 59 FCGGSLISQSWVVTAAHCNVSPGRHFVVLGEYDRSSNAEPLQVLSVSRAITHPSWNSTTM 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57 TCGGSLIANSWVLTAAHCISSSRIYRVMLGQHNLYVAESGSLAVSVSKIVVHKDWNSNOV 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             119 N--NDVTLLKLASPAQYTTRISPVCLASSNEALTEGLTCVTTGWGRLSGVGNVTPAHLQQ 176
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                                                                                                                                                                                                                                                                                                                                                                                                               59 FCGGSLISQSWVVTAAHCNVSPGRHFVVLGEYDRSSNAEPLQVLSVSRAITHPSWNSTTM 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N--NDVTLLKLASPAQYTTRISPVCLASSNEALTEGLTCVTTGWGRLSGVGNVTPAHLQQ 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SNGNDIALVKLASPVALTSKIQTACLPPAGTILPNNYPCYVTGWGRLQTNG-ATPDVLQQ 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MIRTLLLSTLVAG-ALSCGVSTYAPDMS---RMLGGEEARPNSWPWQVSLQYSSNGQWYH 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 177 VALPLVTVNQCRQ--YWDSSITDSMICAGGAGA-SSCQGDSGGPLVCQKGN-TWVLIGI 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            176 GRLLVVDYATCSSSGWWGSTVKTNMICAGGDGVICTCNGDSGGPLNCQASDGRWEVHGI 234
                                                                                                                                                                                                                                                                                                                                   177 VALPLVTVNQC--RQYWDSSITDSMICAGGAG-ASSCQGDSGGPLVCQKGN-TWVLIGI 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A Molecule type: mRNA
A Residues: 1-269 cKAM>
A) Residues: 1-269 cKAM>
A) Residues: 1-269 cKAM>
A) Cross-references: GB: MI6653; NID: 9182059; PIDN: AAA52381.1; PID: 9182060
C; Superfamily: trypsin; trypsin homology
C; Superfamily: trypsin; trypsin prodoctionacs
F; Reynowas: hydrolase; serine proteinase
F; 1-16/Domain: signal sequence #status predicted <PRO>
F; 1-28/Domain: propeptide #status predicted <PRO>
F; 29-26/Product: pancreatic elastrase IIB #status predicted <MAT>
F; 29-26/Zpomain: trypsin homology <TRY>
F; 39-126/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                              2 LLLSLTLSLVLLGSSWGCGIPAIKPALSFSQRIVNGENAVLGSWPWQVSLQD-SSG--FH
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                                                                                                                                                                                                                                       12;
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F;1-16/Domain: signal sequence #status predicted <SIG>
F;17-30/Domain: activation peptide #status predicted <APT>
F;31-271/Product: elastase II #status predicted <MPT>
F;31-264/Domain: trypsin homology <TRY>
F;75,123,218/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Accession: C26823
R;Kawashima, I.; Tani, T.; Shimoda, K.; Takiguchi, Y.
DNA 6, 163-172, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                             35.9%; Score 438; DB 1;
41.8%; Pred. No. 1.2e-29;
tive 36; Mismatches 91
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Pred. No. 1e-28;
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Best Local Similarity 41.8%
Matches 100; Conservative
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Best Local Similarity 41.0*
Matches 98; Conservative
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A.Accession: JX0045
A.Molecule type: mRNA
Residues: 1-240, 'G', 242-270 CSHI>
A.Cross-references: GB:D00306; NID:g220013; PIDN:BAA00212.1; PID:g220014
A.Cross-references: GB:D00306; NID:g220013; PIDN:BAA00212.1; PID:g220014
C.Comment: This enzyme is an alanine-specific serine proteinase that has little elast C.Genetics: 15/1; 43/3; 76/2; 121/2; 16/1; 214/3; 265/3
A.Introns: 15/1; 43/3; 76/2; 121/2; 16/1; 214/3; 265/3
C.Superfamily: trypsin; trypsin homology
C.Keywords: hydrolase; pancreas; serine proteinase
F:1-15/Domain: signal sequence #status predicted <FRO>
F:16-28/Domain: propeptide #status predicted <FRO>
F:29-270/Product: pancreatic clastases IIIA #status experimental <MAT>
F:29-263/Domain: trypsin homology <TRY>
F:29-263/Domain: trypsin homology <TRY>
F:29-283/Domain: Asp. Ser #status predicted
                                C;Species: Homo sapiens (man)
C;Date: 15-Dec-1988 #text_change 20-Jun-2000
C;Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 20-Jun-2000
C;Accession: A29934; JX0045
R;Tani, T.; Ohsumi, J.; Mita, K.; Takiguchi, Y.
J Blol, Chem. 263, 1231-1239, 1988
A;Title: Identification of a novel class of elastase isozyme, human pancreatic elasta A;Reference number: A92664; MUID:880087253; PMID:2826474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:J03516
R;Shirasu, Y.; Takemura, K.; Yoshida, H.; Sato, Y.; Iijima, H.; Shimada, Y.; Mikayama J. Biochem. 104, 259-264, 198
A;Title: Molecular cloning of complementary DNA encoding one of the human pancreatic A;Reference number: JX0045; MUID:89034017; PMID:2460440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SCVACGNDIALIKLSRSAQLGDAVQLASLPPAGDILPNKTPCYITGWGRLYTNGPL-PDK 174
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ternate names: protease E
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1 IVNGENAVPGSWPWQVSLQD......AMYTRVSKFSTWINQVMAYN 231
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/cgn2_6/ptodata/1/laa/6A_COMB.pep:*
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              GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd
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S-08-487-167-10
S-08-296-149-10
S-08-801-499-10
S-08-615-271-10
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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                                                                                                                      Run on:
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Sequence 62, Application US/08944483

Sequence 62, Application US/08944483

Patent No. 6232456

GENERAL INFORMATION:

APPLICANT: COMPATTS, TRACEY L.

APPLICANT: GRAMANOS, EDWARD N.

APPLICANT: STECHANDOS, EDWARD N.

TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS

TITLE OF INVENTION: OP THE PROSTATE

NUMBER OF SEQUENCES: 76

CORRESPONDENCE ADDRESS:
                                            Sequence 54, Appl
Sequence 54, Appl
Sequence 1, Appli
Sequence 1, Appli
Sequence 2, Appli
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   Sequence 5
Sequence 1
Patent No.
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Sequence
Sequence
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US-08-944-483-53
US-09-296-219-12
52003-08-296-219-12
US-08-466-54
US-08-466-54
US-09-131-955-1
US-09-132-154-1
US-09-132-154-1
US-09-132-154-1
US-08-132-154-1
US-08-132-154-1
US-08-132-154-1
US-08-147-0008-29
US-08-514-1
US-08-624-1
US-08-451-932-1
US-08-451-932-1
US-08-451-932-1
US-08-451-932-1
US-08-451-932-1
US-08-451-932-1
US-08-451-932-1
US-08-605-5988-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDION TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,483
                                                                                                                                                                                                                                                                                                                                                ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6183.US.01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEE: Abbott Laboratories
1: 100 Abbott Park Road
Abbott Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 230 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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Tanimoto, Hirotoshi
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TELEFAX: (212) 354-8113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
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: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: New York
STATE: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 10036-2787
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US-08-557-146-13
                                                                                                                                                                                                       SEQ ID NO 6
LENGTH: 231
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                                                                                                                                                                                                                                             TYPE: PRT
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APPLICANT: Tanimoto, Hirotoshi
TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease Overexpressed in
TITLE OF INVENTION: Breast and Ovarian Carcinomas
FILE REFERENCE: D6064
CURRENT APPLICATION NUMBER: US/09/027,337B
CURRENT FILING DATE: 1998-02-20
NUMBER OF SEQ ID NOS: 13
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Serine protease catalytic domain of chymotrypsin (Chymb); OTHER INFORMATION: homologous to similar domain in TADG-15
US-09-027-337-6
                                                                                            1;
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                                                                                                                                                                                                     SNAEPVQVLSIARAITHPNWNANTMNNDLTLLKLASPARYTAQVSPVCLASTNEALPSGL 120
                                                                                                                                                                                                                        TCVTTGWGRISGVGNVTPARLQQVVLPLVTVNQCRQYWGARITDAMICAGGSGASSCQGD 180
                                                                                                                                                                                                                                                                                               120 LCATTGWGKTKYNANKTPDKLQQAALPLLSNAECKKSWGRRITDVWICAGASGVSSCWGD 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 SNAEPVQVLSIARAITHPNWNANTMNNDLTLLKLASPARYTAQVSPVCLASTNEALPSGL 120
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                                                                                            Gaps
                                                                                                                            1 IVNGENAVPGSWPWQVSLQDNTGFHFCGGSLISPNWVVTAAHCQVTPGRHFVVLGEYDRS 60
                                                                                                                                                 1 IVNGEDAVPGSWPWQVSLQDKTGFHFCGGSLISEDWVVTAAHCGVRTS-DVVVAGEFDGG 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 IVNGENAVPGSWPWQVSLQDNTGFHFCGGSLISPNWVVTAAHCQVTPGRHFVVLGEYDRS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59.9%; Score 750.5; DB 2; Length 231; 58.0%; Pred. No. 4.3e-64; ive 35; Mismatches 61; Indels 1
                                                       DB 4; Length 230;
                                                                                                                                                                                                                                                                                                                                                                      SGGPLVCQKGNTWVLIGIVSWGTKNCNIQAPAMYTRVSKFSTWINQVMAYN 231
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                                                                                          61; Indels
                                                   59.9%; Score 750.5; DB 4 58.0%; Pred. No. 4.3e-64; Live 35; Mismatches 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-027-337-6; Sequence 6, Application US/09027337B; Patent No. 5972616
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Patent No. 6451500
GENERAL INFORMATION:
No. 6232456e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: O'Brien, Timothy J.
                                                   Query Match 59.9%
Best Local Similarity 58.0%
Matches 134; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 59.99
Best Local Similarity 58.09
Matches 134; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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ORGANISM: Unknown
; MOLECULE TYPE:
US-08-944-483-62
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121 LCATTGWGKTKYNANKTPDKLQQAALPLLSNAECKKSWGRRITDVMICAGASGVSSCMGD 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 TCVTTGWGRISGVGNVTPARLQQVVLPLVTVNQCRQYWGARITDAMICAGGSGASSCQGD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 IVNGENAVPGSWPWQVSLQDNTGFHFCGGSLISPNWVVTAAHCQVTPGRHFVVLGEYDRS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 13, Application US/08557146
Patent No. 5834290
GENERAL INFORMATION:
APPLICANT: Bealrud, Torbjorn
APPLICANT: Hansson, Lennart
TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
TITLE OF INVENTION: Enzyme (SCCE)
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 SGGPLVCQKGNTWVLIGIVSWGTKNCNIQAPAMYTRVSKFSTWINQVMAYN 231
TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease TITLE OF INVENTION: Overexpressed in Carcinomas FILE REFERENCE: D6064CIP/D
CURRENT APPLICATION WIDER: US/09/644,600
CURRENT FILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: 09/421,213
PRIOR FILING DATE: 1999-10-20
PRIOR FILING DATE: 1999-10-20
PRIOR FILING DATE: 1998-02-20
NUMBER OF SEQ ID NOS: 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/557,146
FILING DATE: 14-DEC-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Sterner, Richard J.
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-181
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 59.9%; Score 750.5; DB 4; Best Local Similarity 58.0%; Pred. No. 4.3e-64; Matches 134; Conservative 35; Mismatches 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: White & Case, Patent Department 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Chymotrypsin US-09-644-600-6
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SNAEPVQVLSIARAITHPNWNANTMNNDLTLLKLASPARYTAQVSPVCLASTNEALPSGL 120
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                                                                                                                               1 IVNGENAVPGSWPWQVSLQDNTGFHFCGGSLISPNWVVTAAHCQVTPGRHFVVLGEYDRS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 IVNGENAVPGSWPWQVSLQDNTGFHFCGGSLISPNWVVTAAHCQVTPGRHFVVLGEYDRS 60
                                                                                                                                                                                                                                                                                     TCVTTGWGRISGVGNVTPARLQQVVLPLVTVNQCRQYWGARITDAMICAGGSGASSCQGD
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                                                                                                                                                                                                                                                                                                                                                                                  181 SGGPLVCQKGNTWVLIGIVSWGTKNCNIQAPAMYTRVSKFSTWINQVMAYN 231
                                                         Length 229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FOC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/278,091
FILING DATE: 21-3UL-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 724.5; DB 1
Pred. No. 1.3e-61;
                                                       Score 737; DB 2;
Pred. No. 8.3e-63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: LOOSMORE, Sheena M
APPLICANT: TANG, Yan-Ping
APPLICANT: CHONG, Pele
APPLICANT: CHONG, Reymond P.
APPLICANT: REIEN, MICHEL H.
TITLE OF INVENTION: Reduced Protease Activity
TITLE OF INVENTION: Reduced Protease Activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Suin & Meburney
STREET: Suite 701, 330 University Avenue
                                                                                            36; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 10, Application US/08278091
Patent No. 5506139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 10:
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                                                     58.9%;
nilarity 57.6%;
Conservative 3
; MOLECULE TYPE: polypeptide US-09-154-344-13
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Best Local Similarity 57.1%
Matches 132; Conservative
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linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
                                                         Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 6
US-08-278-091-10
                                                                                            Matches 133;
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Recombinant Stratum Corneum Chymotryptic
Enzyme (SCCE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 SGGPLVCQKGNTWVLIGIVSWGTKNCNIQAPAMYTRVSKFSTWINQVMAYN 231
                                                                                                                                                                   Length 229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                               11arity 57.6%; Pred. No. 8.3e-63; Conservative 36; Mismatches 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: White & Case, Patent Department
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1103326-181
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APPLICATION NUMBER: US 08/557,146
FILING DATE: 14-DEC-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UMBER: US/09/154,344
16-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 13, Application US/09154344
Patent No. 5981256
GENERAL INFORMATION:
APPLICANT: Egelrud, Torbjorn
APPLICANT: Hansson, Lennart
TITLE OF INVENTION: Recombinant Str
TITLE OF INVENTION: Enzyme (SCCE)
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Sterner, Richard J. REGISTRATION NUMBER: 35,372 REFERENCE/DOCKET NUMBER: 111 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (212) 354 8113
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                   TYPE: amino acids
STRANDEDNESS: single
TOPOLGGY: linear
MOLECULE TYPE: polypeptide
US-08-557-146-13
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TYPE: amino acids
STRANDEDNESS: single
                                     : 229 amino acids
amino acids
INFORMATION FOR SEQ ID NO:
                 SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                             Query Match
Best Local Similarity
Matches 133; Conserv
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'RY: U.S.A.
10036-2787
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US-09-154-344-13
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                                 LENGTH:
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61 SNAEPVQVLSIARAITHPNWNANTMNNDLTLLKLASPARYTAQVSPVCLASTNEALPSGL 120
SNAEPVQVLSIARAITHPNWNANTMNNDLTLLKLASPARYTAQVSPVCLASTNEALPSGL 120
                     TCVTTGWGRISGVGNVTPARLQQVVLPLVTVNQCRQYWGARITDAMICAGGSGASSCQGD 180
                                                                                                       1 IVNGEEAVPGSWPWQVSLQDKTGFHFCGGSLINENWVVTAAHCGVTTS-DVVVAGEFDQG 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 IVNGENAVPGSWPWQVSLQDNTGFHFCGGSLISPNWVVTAAHCQVTPGRHFVVLGEYDRS 60
                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: CHONG, Pele
APPLICANT: OOMEN, Raymond P.
APPLICANT: OOMEN, Raymond P.
TITLE OF INVENTION: Analog of Haemophilus Hin47 Protein with
TITLE OF INVENTION: Reduced Protease Activity
UNDBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 228;
                                                                                                                                                                             SGGPLVCQKGNTWVLIGIVSWGTKNCNIQAPAMYTRVSKFSTWINQVMAYN 231
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,173
FILING DATE: 07-JUN-1995
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Pred. No. 1.3e-61
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Suite 701, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1038-493 MIS:vg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/296,149
FILING DATE: 26-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/278,091
FILING DATE: 21-JUL-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                        Sequence 10, Application US/08472173 Patent No. 5665353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Stewart, Michael I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038
TELECOMMUNICATION INFORMATION:
TELEPAN: (416) 595-1155
TELEPAN: (416) 595-1163
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                              APPLICANT: LOOSMORE, Sheena M APPLICANT: YANG, Yan-Ping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57.9%;
57.1%;
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Best Local Similarity 57.1%
Matches 132; Conservative
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MEDIUM TYPE: Floppy
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M5G 1R7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: Suite 70
CITY: Toronto
STATE: Ontario
                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: LOOSMO
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 61
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                                         61 SNAEPVQVLSIARAITHPNWNANTMNNDLTLLKLASPARYTAQVSPVCLASTNEALPSGL 120
                                                               121 TCVTTGWGRISGVGNVTPARLQQVVLPLVTVNQCRQYWGARITDAMICAGGSGASSCQGD 180
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   1 IVNGEEAVPGSWPWQVSLQDKTGFHFCGGSLINENWVVTAAHCGVTTS-DVVVAGEFDQG 59
                                                                                                                                           3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Analog of Haemophilus Hin47 Protein with TITLE OF INVENTION: Reduced Protease Activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 228;
                                                                                                                                                                                                                       SGGPLVCQKGNTWVLIGIVSWGTKNCNIQAPAMYTRVSKFSTWINQVMAYN 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,859
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/296,149
FILING DATE: 26-AUG-1994
PRIOR APPLICATION NUMBER: US 08/296,149
FILING DATE: 21-JUL-1994
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Score 724.5; DB 1
; Pred. No. 1.3e-61;
34; Mismatches 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 1038-495 MIS:V9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                            Sequence 10, Application US/08483859
Patent No. 5656436
GENERAL INFORMATION:
APPLICANT: LOOSMORE, Sheena M.
APPLICANT: YANG, Yan-Ping
APPLICANT: CHONG, Pele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24,973
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: YANG, Yan-Ping
APPLICANT: CHONG, Pele
APPLICANT: COMEN, Raymond P.
APPLICANT: KLEIN, Michel H.
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57.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 23
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ADDRESSEE: Sim & MCB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
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Best Local Similarity
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COMPUTER: IB
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US-08-483-859-10
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NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 228 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best_Local Similarity 57.1
Matches 132; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: Suite 701
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
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US-08-482-816-10
                                                                                                                                                                           RESULT 10
US-08-482-816-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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SNAEPVQVLSIARAITHPNWNANTMNNDLTLLKLASPARYTAQVSPVCLASTNEALPSGL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of Haemophilus Hin47 Protein with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 228;
                                                                                                                                          SGGPLVCQKGNTWVLIGIVSWGTKNCNIQAPAMYTRVSKFSTWINQVMAYN 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,167
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: LOCSMORE, Sheena M.
APPLICANT: TANG, Yan-Ping
APPLICANT: CHONG, Pele
APPLICANT: CHONG, Pele
APPLICANT: CHONG, Raymond P.
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: Analog of Haemophilus Hin47
ITLE OF INVENTION: Reduced Protease Activity
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 57.9%; Score 724.5; DB 2; Best Local Similarity 57.1%; Pred. No. 1.3e-61; Matches 132; Conservative 34; Mismatches 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 1038-508 MIS:vg
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION: 433
PRIOR APPLICATION 1433
APPLICATION NUMBER: US 08/296,149
FILING DATE: 26-NUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/278,091
FILING DATE: 21-JUL-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                              Sequence 10, Application US/08487167
Patent No. 5869302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Stewart, Michael I.
REGISTRATION NUMBER: 24,973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 228 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRY: Canada
M5G 1R7
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STATE: Ontario
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Analog of Haemophilus Hin47 Protein with Reduced Protease A
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1 IVNGENAVPGSWPWQVSLQDNTGFHFCGGSLISPNWVVTAAHCQVTPGRHFVVLGEYDRS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 228;
                                                                                               181 SGGPLVCQKGNTWVLIGIVSWGTKNCNIQAPAMYTRVSKFSTWINQVMAYN 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,816
FILING DATE: 07-JUN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/296,149
FILING DATE: 26-AUG-1994
PRIOR APPLICATION NUMBER: US 08/278,091
FILING DATE: 21-JUL-1994
ATTONINY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57.9%; Score 724.5; DB 2;
57.1%; Pred. No. 1.3e-61;
11ve 34; Mismatches 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Suite 701, 330 University Avenue
                                                                                                                                                                                                                                           Sequence 10, Application US/08482816
Patent No. 5935573
                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: LOOSMORE, Sheena M
APPLICANT: TANG, Yan-Ping
APPLICANT: CHONG, Pele
APPLICANT: CHONG, Pele
APPLICANT: CHONGN, Raymond P.
APPLICANT: CHONGN, Raymond P.
APPLICANT: CLEIN, Michel H.
TITLE OF INVENTION: Analog of
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: SIM & MCBULNEY
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STATE: Ontario
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US-08-801-499-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 TCVTTGWGRISGVGNVTPARLQQVVLPLVTVNQCRQYWGARITDAMICAGGSGASSCQGD 180
120 TCVTTGWG-LTRYAN-TPDRLQQASLPLLSNTNCKKYWGTKIKDAMICAGASGVSSCMGD 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 IVNGEEAVPGSWPWQVSLQDKTGFHFCGGSLINENWVVTAAHCGVTTS-DVVVAGEFDQG 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 IVNGENAVPGSWPWQVSLQDNTGFHFCGGSLISPNWVVTAAHCQVTPGRHFVVLGEYDRS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |::| :| || || :: : :|: ||:|||:|||||: : :| SSSEKIQKLKIAKVFKNSKYNSLTINNDITLIKLSTAASFSQTVSAVCLPSASDDFAAGT
                                                                                                                                                                                                                 APPLICANT: LOOSMORE, Sheena M
APPLICANT: YANG, Yan-Ping
APPLICANT: CHONG, Pele
APPLICANT: CHONG, Pele
APPLICANT: RAEIN, Michel H.
TITLE OF INVENTION: Raduced Protease Activity
NUMBER OF SEQUENCES: 23
                                   COMPUTER READABLE FORM:
MEDIOW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/296,149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62;
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Best Local Similarity 57.1%; Pred. No. 1.3e-61;
                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34; Mismatches
                                                                                                                                                          Sequence 10, Application US/08296149 Patent No. 5939297 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 103
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              228 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS ADDRESSEE: Sim & MCF
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US-08-296-149-10
                                                                                                                                           US-08-296-149-10
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                                   181
                                                                      178
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APPLICANT: YANG, Yan-Ping
APPLICANT: CHONG, Pele
APPLICANT: CHONG, Pele
APPLICANT: Michel H.
TITLE OF INVENTION: Analog of Haemophilus Hin47 Protein with Reduced Protease A
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/801,499
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57.9%; Score 724.5; DB 57.1%; Pred. No. 1.3e-61
                                                                                                                                                                                                                                                              ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
CITY: Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 08/278,091
FILING DATE: 1-70L-1994
ATORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRANTON NUMBER: 24,993
REFERENCE/DOCKET NUMBER: 1038-671 MIS:jb
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/482,816
FILING DATE: 07-UN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/296,149
FILING DATE: 26-AUG-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US 08/278,091
Sequence 10, Application US/08801499
Patent No. 5962430
GENERALINFORMATION:
APPLICANT: LOOSMORE, Sheena M
                                                                                                                                                                                                                                                                                                                                                                                                                                                        IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPRAN: (416) 595-1155
TELEPRAN: (416) 595-1163
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 228 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                  Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 57.9%
Best Local Similarity 57.1%
Matches 132; Conservative
                                                                                                                                                                                                                                                                                                                                                           COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: sil
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RESULT 13

RESULT 12

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SNAEPVQVLSIARAITHPNWNANTMNNDLTLLKLASPARYTAQVSPVCLASTNEALPSGL 120
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            Analog of Haemophilus Hin47 Protein with
Reduced Protease Activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 3; Length 228;
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                                                                                                                                                                                                                                                                                                             PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57.9%; Score 724.5; DB 3
illarity 57.1%; Pred. No. 1.3e-61;
Conservative 34; Mismatches 62
                                                                                            ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1038-731 MIS: Jb
                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/487,167
FILING DATE: 07-UN-1995
PRIOR APPLICATION NUMBER: US 08/296,149
FILING DATE: 26-AUG-1994
FILING DATE: 26-AUG-1994
PRIOR APPLICATION NUMBER: US 08/278,091
FILING DATE: 21-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-731 MI
                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/074,660
                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 10, Application US/09074659
Patent No. 6025342
GENERAL INFORMATION:
APPLICANT: LOOSMORE, Sheena M.
APPLICANT: VANG, Yan-Ping
APPLICANT: CHONG, Pele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 10:
KLEIN, Michel H.
                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        single
                                                        NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                 TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
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Matches 132; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                      M5G 1R7
                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY:
US-09-074-660-10
                                                                                                                                                                                                                                                                                                                SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-074-659-10
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                                                                     APPLICANT: LOOSMORE, Sheena M.
APPLICANT: YANG, Yan-Ping
APPLICANT: CHONG, Pele
APPLICANT: OCHEN, Pele
APPLICANT: OCHEN, Raymond P.
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: ANALOG OF HAEMOPHILUS HIN47 WITH REDUCED
TITLE OF INVENTION: PROTEASE ACTIVITY
WUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SGGPLVCQKGNTWVLIGIVSWGTKNCNIQAPAMYTRVSKFSTWINQVMAYN 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                  SUFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/615,271
FILING DATE: 30-JUN-1996
CLASSIFICATION: 514
ATTORNEY/AGENT ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57.9%; Score 724.5; DB 2
57.1%; Pred. No. 1.3e-61;
tive 34; Mismatches 62
                                                                                                                                                                                                                                                              E: Sim & McBurney
6th Floor, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 10, Application US/09074660 Patent No. 6020183
            Sequence 10, Application US/08615271
Patent No. 5981503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 228 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: LOOSMORE, Sheena M. APPLICANT: YANG, Yan-Ping APPLICANT: CHONG, Pele APPLICANT: OOMEN, Raymond P.
                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24,973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 57.1%
Matches 132; Conservative
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                                                                                                                                                                                                                                                                                    STREET: 6th Floc
CITY: Toronto
STATE: Ontarlo
                                                                                                                                                                                                                                                                                                                                                COUNTRY: Canada
ZIP: MSG 1R7
                                                     GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-615-271-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3;
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: Analog of Haemophilus Hin47 Protein with
TITLE OF INVENTION: Reduced Protease Activity
NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 SGGPLVCOKGNTWVLIGIVSWGTKNCNIQAPAMYTRVSKFSTWINQVMAYN 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62; Indels
                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/074,659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 724.5; DB 3 Pred. No. 1.3e-61;
                                                                     CONTRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
CITY: Toronto
STATE: Ontario
CONTRY: Canada
ZIP: MSG 1H7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57.9%; Scor.
57.1%; Pred. No. 1....
34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1038-730 MIS: 1b
                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION:
APPLICATION NUMBER: US 08/487,167
FILING DATE: 07-20N-1995
FILING DATE: 07-20N-1995
APPLICATION NUMBER: US 08/296,149
FILING DATE: 26-NG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/278,091
FILING DATE: 21-70L-1994
FILING DATE: 21-70L-1994
ATTORNEY, AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Stewart, Michael I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038
TELECOMMUNICATION INFORMATION:
TELEFAX: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 228 maino acids
TYPE: amino acid
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 57.1%
Matches 132; Conservative
                                                                                                                                                                                                                                                                                                                                                                   FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY:
US-09-074-659-10
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Search completed: December 20, 2002, 15:20:39 Job time: 14.087 secs

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P27435 P00762 P00762 P00343 P009148 P009148 P00914 P006871 P006871 P006872 P00773 P007

MCT7_RAT MCT6_RAT MCT6_RAT TMS2_MOUSE TRX1_CHICK TRX1_CHICK TRX2_CHICK TRX2_CHICK TRX2_CANFA TRX2_CANFA TRX2_CANFA TRX2_CANFA TRX2_CANFA TRX2_CANFA TRX2_CANFA MCT6_MOUSE

442.5 439.5 439.5 439.5 439.5 430.5 430.5 430.5

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December 20, 2002, 15:12:58 ; search time 7.91304 Seconds (without alignments) 1210.790 Million cell updates/sec
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 version 5.1.3
- 2002 Compugen Ltd
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                                                                                                                                                                                  US-09-856-319B-4_COPY_34_264
1252
1 IVNGENAVPGSWPWQVSLQD.....
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Maximum Match 100%
Listing first 45 summaries
                                                                         OM protein - protein search, using sw model
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GenCore
Copyright (c) 1993
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Maximum DB seq length: 200000000
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                                                                                                                                                                                    Title:
Perfect score:
                                                                                                                                                                                                                                                             Scoring table:
                                                                                                                                                                                                                                                                                                                                                        Total number
                                                                                                                                                                                                                       Sequence:
                                                                                                                                                                                                                                                                                                                   Searched:
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                                                                                                             Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	ŭ	Query Match	Query Match Length DB	DB	ID	Description	
-	1119	4.68	264		CTRL HUMAN	P40313 homo sai	Santen
~	757.5	60.5	263	-	CHES CANED	atueo	111111111111111111111111111111111111111
m	750.5	6.65	263	-	CTRA GADMO		orhu
4	750.5	59.9	263	٦	CTRB_HUMAN		pten
'n	740.5	59.1	245		CTRB_BOVIN		rus
ø	727.5	58.1	245	Н	CTRA_BOVIN	P00766 bos taurus	rus
7	715.5	57.1	263	Н	CTRB_RAT	P07338 rattus norv	norv
œ	714.5	57.1	245	7	CTRB_GADMO	P80646 gadus morhu	orhu
6	503	40.2	269	٦	EL2_PIG	P08419 sus scrofa	ofa
10	499	39.9	271	ч	EL2_RAT	P00774 rattus norv	norv
11	497.5	39.7	253	٦	CAC3_BOVIN	P05805 bos taurus	rus
12	486	38.8	269	~	EL2A_HUMAN	_	pien
13	481.5	38.5	270	٦	EL3B_HUMAN	_	pien
14	480	38.3	269	-	EL2 BOVIN		rus
15	475	37.9	271	٦	EL2_MOUSE	_	culu
16	464.5	37.1	810	٦	PLMN_HUMAN	P00747 homo sapien	pien
17	462	36.9	812	П	PLMN_MOUSE	P20918 mus musculu	culu
18	459.5	36.7	270	П	EL3A_HUMAN	P09093 homo sapien	pien
19	455.5	36.4	270	-	TRYT_MERUN	P50342 meriones un	un s
20	455.5	36.4	342	٦	PSS8_RAT	Q9es87 rattus norv	norv
21	455	36.3	454	П	TMS3_HUMAN	P57727 homo sapien	pien
22	452.5	36.1	275	Н	TRYT_PIG	٠,	ofa
23	452.5	36.1	343	Н	PLMN_SHEEP		ies
24	451.5	36.1	810	-	PLMN_MACMU	P12545 macaca mula	mula
25	449.5	35.9	790		PLMN_PIG	P06867 sus scrofa	ofa
56	449	35.9	269	Н	EL2B_HUMAN	P08218 homo sapien	pien
27	448.5	35.8	333	Н	PLMN CANFA	P80009 canis famil	amil
28	448.5	35.8	343	Н	PSS8_HUMAN	016651 homo sapien	pien
53	447.5	35.7	268		CLCR_HUMAN	099895 homo sapien	pien
30	447.5	35.7	268		CLCR RAT		norv
31	447.5	35.7	273	Н	MCT7_MOUSE	_	musculu
32	447.5	35.7	342	-	PSS8 MOUSE	SIL	musculu
33	444	35.5	231	-	TRYP_PIG	Sns	scrofa

SULT 1 RL_HUMAN	CTRL OR CTRL1. Homo sapiens (Human). Eukaryota: Metazoa; Chordat Mammalia; Eutheria; Primate (CBI_TaxID=9606;	RP SEQUENCE FROM N.A RX MEDLINE-94093544; PubMed-8268911; RX MEDLINE-95093544; PubMed-8268911; RA Larsen F., Solheim J., Kristensen T., Kolsto A.B., RT A tight cluster of five unrelated human genes on	RT 1642.1."; RL Hum. Mol. Genet. 2:1589-1595(1993). CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.			use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license acreement (See http://www.isb-sib.ch/announce)			EMBL; X71877; CAA50711.1;	MEROPS; S01.256;		InterPro; IPR001314; InterPro; IPR001254;		SMART; SM00020; Tryp_SPC; 1.	PROSITE: PS50240; TRYPSIN_DOM;	PROSITE; PS00134, INTESTMENT PROSITE; PS00135; TRYPSIN_SE	Hydrolase; Serine protease; Gly SIGNAL	PROPEP 19 33 • CHAIN 34 264	ACT_SITE 75 75	121	CARBOHYD 114 114 N-L	FT DISULFID 19 141 BY SIMILARITY. FT DISULFID 60 76 BY SIMILARITY.		
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                                                                                                                                                                                                                                                                                                                                                             TCVTTGWGRISGVGNVTPARLQQVVLPLVTVNQCRQYWGARITDAMICAGGSGASSCQGD 180
                                                                                                                                                                                                                                                SNAEPVQVLSIARAITHPNWNANTMNNDLTLLKLASPARYTAQVSPVCLASTNEALPSGL 120
                                                                                                               Gaps
                                                                                                                                                                               1 IVNGENAVPGSWPWQVSLQDNTGFHFCGGSLISPNWVVTAAHCQVTPGRHFVVLGEYDRS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATALYTIC ACTIVITY: Preferential cleavage: Tyr-|-Xaa, Trp-|-Xaa,
Phe-|-Xaa, Leu-|-Xaa.
SUBCELLULAR LOCATION: Extracellular.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE-84170253; PubMed-6584866;
Pinsky S.D., Laforge K.S., Luc V., Scheele G.;
"Identification of cDNA clones encoding secretory isoenzyme forms:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Ćhordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
NCBL_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR001254; Ser_protease_Try.
PRIMTS; PR00022; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPc; 1.
SMART; SM00020; TRYPSIN_LOM; 1.
PROSITE; PS00134; TRYPSIN_LS; 1.
PROSITE; PS00135; TRYPSIN_LS; 1.
PROSITE; PS00135; TRYPSIN_LSR; 1.
PROSITE; PS00135; TRYPSIN_LSR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence determination of canine pancreatic prechymotrypsinogen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 264;
                                                                                                                                                                                                                                                                                                                                                                                                                              SGGPLVCQKGNTWVLIGIVSWGTKNCNIQAPAMYTRVSKFSTWINQVMAYN 231
                                                                                                            10; Indels
                    3F629F02FA6DDFB4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHYMOTRYPSIN 2, A CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Natl. Acad. Sci. U.S.A. 80:7486-7490(1983)
                                                                89.4%; Score 1119; DB 1; 86.1%; Pred. No. 3.1e-93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHYMOTRYPSINOGEN 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-AUG-1987 (Rel. 05, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Chymotrypsinogen 2 precursor (EC 3.4.21.1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       263 A.A.
                                                                                                            22; Mismatches
  BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-AUG-1987 (Rel. 05, Created)
                    28002 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; K01173; AAA30841.1; -.
                                                                                                            Matches 199; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Canis familiaris (Dog).
210 ,
264 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; A21195; A21195
HSSP; P00766; 1ACB.
                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEROPS; S01.152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTR2_CANFA P04813;
DISULFID
SEQUENCE
                                                                   Query Match
                                                                                          Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            SNAEPVQVLSIARAITHPNWNANTMNNDLTLLKLASPARYTAQVSPVCLASTNEALPSGL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCVTTGWGRISGVGNVTPARLOQVVLPLVTVNQCRQYWGARITDAMICAGGSGASSCQGD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            153 LCVTTGWGLTKHTNANTPDKLQQAALPLLSNAECKKFWGSKITDLMVCAGASGVSSCMGD 212
                                                                                                                                                                                                                                                                                                                                                               MEDLINE-92111252; PubMed-1764912;
Asgeirsson B., Bjarnason J.B.;
Astroctural and kinetic properties of chymotrypsin from Atlantic cod (Gadus morhua). Comparison with bovine chymotrypsin.";
Comp. Biochem. Physiol. 99B:327-335(1991).
-!- CATALYTIC ACTIVITY: Preferential cleavage: Tyr-|-Xaa, Trp-|-Xaa,
                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Gadus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bjarnason J.B.;
"Atlantic cod cDNA encoding a psychrophilic chymotrypsinogen.";
Blochim. Blophys. Acta 1219:211-214(1994).
                                                                                                                                                                                                                                                                                                                       1;
                                                                                                                                                                                                                                                                           Length 263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SGGPLVCQKGNTWVLIGIVSWGTKNCNIQAPAMYTRVSKFSTWINQVMAYN 231
                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gudmundsdottir A., Oskarsson S., Eakin A.E., Craik C.S.,
CHYMOTRYBSIN 2, B CHAIN.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                          SIMILARITY.
2A2F449D813B3961 CRC64;
                                                                                                                                                                                                                                                                           DB 1;
                                                                                                                                                                                                                                                                                                                     61;
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-!- SUBCELLULAR LOCATION: Extracellular.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
                                                                                                                                                                                                                                                      Score 757.5; DB 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Chymotrypsin A precursor (EC 3.4.21.1).
                                                                                                                                                                                                                                                                                                  ; Pred. No. 7.7e 35; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Pyloric caeca;
MEDLINE-94368860; PubMed-8086467;
                                                                                                                                                                                                                               27787 MW;
                                                                                                                                                                                                                                                                           60.5%; ; ; 58.0%; ; ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 19-30 AND 34-49.
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                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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120
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140
76
219
2200
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60
154
186
209
263 AA;
                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                       Matches 134;
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                           CHAIN
ACT_SITE
ACT_SITE
ACT_SITE
DISULFID
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                                                                                                                                                                                                            DISULFID
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Best Local
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Biochem. Biophys. Res. Commun. 158:569-575(1989).
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ACT_SITE
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DISULFID
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CTRB_BOVIN
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                                                                                                                                                                                                                                                                          1;
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                                                                                                                                                                                                                                                                                                                                 121 TCVTTGWGRISGVGNVTPARLQQVVLPLVTVNQCRQYWGARITDAMICAGGSGASSCQGD 180
                                                                                                                                                                                                                                                                                                                         61 SNAEPVQVLSIARAITHPNWNANTMNNDLTLLKLASPARYTAQVSPVCLASTNEALPSGL 120
                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                               SIMILARITY).
SIMILARITY).
SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                    InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR00125; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPC; 1.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS50214; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HS; 1.
PROSITE; PS00135; TRYPSIN_LSR; 1.
Hydrolase; Serine protease; Digestion; Pancreas; Zymogen; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Pancreas;
MEDINE-891347064; PubMed-2917002;
Tomita N., Izumoto Y., Horil A., Doi S., Yokouchi H., Ogawa M.,
Mori T., Matsubara K.;
"Molecular cloning and nucleotide sequence of human pancreatic
                                                                                                                                                                                                                                                        DB 1; Length 263;
                                                                                                                                                                                                                                                                                                                                                                                         SGGPLVCQKGNTWVLIGIVSWGTKNCNIQAPAMYTRVSKFSTWINQVMAYN 231
                                                                                                                                                                                                                                                                                                                                                                                                 62; Indels
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(BY
                                                                                                                       CHYMOTRYPSIN A.
CHARGE RELAY SYSTEM (
CHARGE RELAY SYSTEM (
CHARGE RELAY SYSTEM (
                                                                                                                                                                                                                                                        ; Score 750.5; DB 1; Pred. No. 3.3e-60; 33; Mismatches 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
CTMUMCTYPSINGGEN B PRECURSOR (EC 3.4.21.1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   263 AA.
send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                        28294 MW;
                                                                                                                                                                                                                                                        59.9%;
58.4%;
               EMBL; X78490; CAA55242.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      prechymotrypsinogen cDNA.";
                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                      263
120
120
120
213
220
238
238
24
44
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                                                                                                                                                                                               21
25
29
44
46
263 AA;
                                                                                                                                                                                                                                                                Similarity
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                               MEROPS; S01.152;
                                                                                                                                                      19
60
154
186
209
                        P00766;
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P17538;
                                                                                                                                                                                                                                                                         Matches 135;
                                                                                                                                      ACT_SITE
ACT_SITE
DISULFID
                                                                                                                                                                                                       CONFLICT
CONFLICT
CONFLICT
CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 TCVTTGWGRISGVGNVTPARLQQVVLPLVTVNQCRQYWGARITDAMICAGGSGASSCQGD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 IVNGENAVPGSWPWQVSLQDNTGFHFCGGSLISPNWVVTAAHCQVTPGRHFVVLGEYDRS 60
                                           Strausberg R.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: Preferential cleavage: Tyr-|-Xaa, Trp-|-Xaa,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHYMOTRYPSIN B, A CHAIN.
CHYMOTRYPSIN B, B CHAIN.
CHYMOTRYPSIN B, C CHAIN.
CHAMCE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHYMOTRYPSINOGEN B
                                                                                                      Phe-|-Xaa, Leu-|-Xaa.
-!- SUBCELLULAR LOCATION: Extracellular.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59.9%; Score 750.5; DB 1
58.0%; Pred. No. 3.3e-60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MIM; 118890; -.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27870 MW;
                                                                                                                                                                                                                                                                                                                                                        EMBL; M24400; AAA52128.1; -.
                                                                                                                                                                                                                                                                                                                                                                            EMBL; BC005385; AAH05385.1;
PIR; A31299; A31299.
HSSP; P00766; 1CHG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       MEROPS; S01.152; -. Genew; HGNC:2521; CTRB1.
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SEQUENCE FROM N.A.
                        IISSUE-Pancreas;
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19
167
175
175
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209
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REVISION TO 102.
                                                                                  NCBI_TaxID=9913;
                                                                                                                                                                                                                                             Hartley B.S.;
                                                                                                                                                                                                                                                                                                                                                ACTIVE SITE
                                                                                                                                                                                                          chymotry
1;
                                                                                                           SEQUENCE, DISULFIDE BONDS, AND ACTIVE SITE.
MEDILME-68138908; bubMed=5649671;
Smillie L.B., Furka A., Magabhushan N., Stevenson K.J., Parkes C.O.;
"Structure of chymotrypsinogen B compared with chymotrypsinogen A and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 SNAEPVQVLSIARAITHPNWNANTMNNDLTLLKLASPARYTAQVSPVCLASTNEALPSGL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 TCVTTGWGRISGVGNVTPARLQQVVLPLVTVNQCRQYWGARITDAMICAGGSGASSCQGD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tryppinogen.";
Nature 218:343-346(1968).
-!- CATALYTIC ACTIVITY: Preferential cleavage: Tyr-|-Xaa, Trp-|-Xaa,
                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                          Phe-|-xaa, Leu-|-xaa.
-!- SUBCELLULAR LOCATION: Extracellular.
-!- SIMILARIYE'S BELONGS TO PEPTIDASE FAMILY S1.
-!- DATABASE: NAME=Worthington enzyme manual;
--- WWW-hittp://www.worthington-biochem.com/manual/C/CHY.html".
                                                                                                                                                                                                                                                                                                                                                                                                                                                         59.1%; Score 740.5; DB 1; Length 245; larity 57.1%; Pred. No. 2.4e-59; Conservative 32; Mismatches 66; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 SGGPLVCQKGNTWVLIGIVSWGTKNCNIQAPAMYTRVSKFSTWINQVMAYN 231
                                                                                                                                                                                                                                                                                                                                     CHYMOTRYPSIN B, A CHAIN.
CHYMOTRYPSIN B, B CHAIN.
CHYMOTRYPSIN B, C CHAIN.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                         25755 MW; 678016446FF5FEB5 CRC64;
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SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS50240; TRYPSIN_LOM; 1.
PROSITE; PS00114; TRYPSIN_HIS; 1.
PROSITE; PS001135; TRYPSIN_SER; 1.
Hydrolase; Serine protease; Digestion; Pancreas;
                21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
245 AA
                                                                                                                                                                                                                                                 InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_fry.
Pfam; PF00089; trypsin; 1.
PRT:
                                            Chymotrypsinogen B (EC 3.4.21.1).
STANDARD;
                                                                                                                                                                                                                         PIR; A00953; KYBOB.
                                                                                                                                                                                                                                  P00766; 1ACB.
                                                       Bos taurus (Bovine)
                                                                                                                                                                                                                                                                                                                                                                                                                                         245 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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168
191
CTRB_BOVIN
P00767;
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CTRA_BOVIN
ID CTRA_BOVIN
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Matches 132;
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AA 245

PRT;

STANDARD;

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Cohen G.H., Silverton E.W., Davies D.R.;
"Refined crystal structure of gamma-chymotrypsin at 1.9-A resolution.
Comparison with other pancreatic serine proteases.";
J. Mol. Biol. 148:449-479(1981).
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"Structure of alpha-chymotrypsin refined at 1.68-A resolution.";
"J. Mol. Biol. 184:703-711(1985).
-!- CATALYTIC ACTIVITY: Preferential cleavage: Tyr-|-Xaa, Trp-|-Xaa,
21-JUL-1986 (Rel. 01, Created)
15-JUL-1986 (Rel. 01, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Chymotrypsinogen A (EC 3.4.21.1).
Bost tarunus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea;
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MEDLINE=70177557; PubMed=5442169;
Freer S.T., Kraut J., Robertus J.D., Wight H.T., Xuong N.H.;
"Chymotrypsinogen: 2.5-A crystal structure, comparison with alpha-
chymotrypsin, and implications for zymogen activation.";
Biochemistry 9:1997-2009(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brown J.R., Hartley B.S.;
"Location of disulphide bridges by diagonal paper electrophoresis.
The disulphide bridges of bovine chymotrypsinogen A.";
Biochem. J. 101:214-228(1966).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE, AND DISULFIDE BONDS.

BEDILINE-57183948; PubMed-5972866;
Meloun B., Kluh I., Kostka V., Moravek I., Prusik Z., Vanacek J.,
Keil B., Sorm F.;
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"I. Serine proteinases. The structure of alpha-chymotrypsin.";
Philos. Trans. R. Soc. Lond., B. Biol. Sci. 257:67-76(1970).
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MEDLINE-86011575; Pubmed-4046030;
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MEDLINE-82078042; Pubmed-6914398;
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Smillie L.B., Hartley B.S.;
"Histidine sequences in the active centres of some 'serine'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          oŧ
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Blow D.M., Birktoft J.J., Hartley B.S.;
"Role of a buried acid group in the mechanism of action
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Amino-acid sequence of bovine chymotrypsinogen-A.";
Nature 201:1284-1287(1964).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Covalent structure of bovine chymotrypsinogen A.";
Biochim. Biophys. Acta 130:543-546(1966).
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-!- SUBCELLULAR LOCATION: Extracellular.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
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Biochem. J. 101:232-241(1966).
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                                                                                                                                                                                                                                                                                             Bovidae; Bovinae; Bos.
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DATABASE: NAME-Worthington enzyme manual;
WWW-"http://www.worthington-biochem.com/manual/C/CHY.html".
A00952; KYBOA.
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CHYMOTRYPSIN A, B CHAIN.
CHYMOTRYPSIN A, C CHAIN.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
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5CHA, 16-0CT-87

1CHG, 27-JAN-84

1CHO, 16-0CT-87

3GCH, 15-0CT-90

4GCH, 15-0CT-90

4GCH, 15-0CT-90

6GCH, 15-0CT-90

6GCH, 15-0CT-91

1GCH, 22-JUN-94

1GHB, 22-JUN-94

1GCH, 22-JUN-97

1ACC, 12-NOV-97

1ACC, 12-NOV-97

1ACC, 12-NOV-97

1ACC, 12-NOV-97

1ACC, 12-NOV-97
           2; KYBOA.
15-APR-90.
31-MAY-84.
29-OCT-85.
16-OCT-87.
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61 SNAEPVQVLSIARAITHPNWNANTMNNDLTLLKLASPARYTAQVSPVCLASTNEALPSGL 120
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDIZINE-85054881; PubMed-6209274;
Bell G.I., Quinto Ç., Quiroga M., Valenzuela P., Craik C.S.,
Rutter W.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Isolation and sequence of a rat chymotrypsin B gene.";
                                                                                                                                                                                                                                                                                                                                               25666 MW; 91A9F28E2F3E3142 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTRB_RAT STANDARD; PRT; 263 AA. P07338; 01-APR-1988 (Rel. 07, Created) 01-APR-1988 (Rel. 07, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Chymotrypsinogen B precursor (EC 3.4.21.1). CTRB1.
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235
245 AA;
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Query Match
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245 AA;
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J. Biol. Chem. 259:14265-14270(1984).
-!- CATALKTIC ACTIVITY: Preferential cleavage: Tyr-|-Xaa, Trp-|-Xaa,
                                                                                                                                                                                                                                                                                                       CHYMOTRYPSIN B, A CHAIN.
CHYMOTRYPSIN B, B CHAIN.
CHYMOTRYPSIN B, C CHAIN.
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
BY SIMILARITY.
WARABACFRCADAGD CRC64;
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                                                                                                                                                                                                                     PRINTS; PRO072; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPc; 1.
SMART; SF502040; TRYPSIN_LDOM; 1.
PROSITE; PS00134; TRYPSIN_LS; 1.
PROSITE; PS00135; TRYPSIN_LS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gadus morhua (Atlantic cod).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
                                                                                                                                                                                                                                                                                                                                                                                                                                            57.1%; Score 715.5; DB 1; Length 263; 55.4%; Pred. No. 4.5e-57;
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                    Phe-|-Xaa, Leu-|-Xaa.
-!- SUBCELLULAR LOCATION: Extracellular.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.
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01-0cT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Chymotrypsin B (EC 3.4.21.1).
Gadus morhua (Atlantic cod).
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InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
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219 B
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27849 MW; L
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HSSP; P00766; 1CHG.
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Best Local Similarity
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P80646;
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CTRB_GADMO
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TISSUE=Pyloric caeca;
MEDLINE=96439045; PubMed=8841380;
Leth-Larsen R., Asgeirsson B., Thorolfsson M., Noerregaard-Madsen M.,
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Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Gadus.
NCBL_TaxID=8049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 IVNGENAVPGSWPWQVSLQDNTGFHFCGGSLISPNWVVTAAHCQVTPGRHFVVLGEYDRS
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CHYMOTRYPSIN B, B CHAIN.
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  178 QGDSGGPLVCQKGNTWVLIGIVSWGTKNCNIQAPAMYTRVSKFSTWINQVMAYN 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            245;
                                                                                                                                                                                                                  Structure of chymotrypsin variant B from Atlantic cod, Gadus
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InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR001252; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPC; 1.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS00134; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00134; TRYPSIN_SER; 1.
Hydrolase; Serine protease; Digestion; Pancreas; Zymogen.
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OVT -> VIS (IN REF. 2).

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WHY 74 FEOD425517AB02 CRC64;
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Pred. No. 5.1
                                                                                                                                                                                                                                                            Biochim. Biophys. Acta 1297:49-56(1996)
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55.1%;
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230 YN 231
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  Query Match
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P00774:
                Best Local
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                                                                                                                                                                                                                                                                                                                                                                                  -i- FUNCTION: ACTS UPON ELASTIN.
-i- CATALYTIC ACTIVITY: Preferential cleavage: Leu-|-Xaa, Met-|-Xaa
                                                                                                                                                                                                                                                                                                                                                                                                                                          -i- TISSUE SPECIFICITY: PANCREAS.
-i- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. ELASTASE SUBFAMILY.
                                                                                                                                                                                      Kawashima I., Tani T., Shimoda K., Takiguchi Y., Characterization of pancreatic elastase II cDNAs: two elastase II mRNAs are expressed in human pancreas.";
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SIMILARITY).
SIMILARITY).
                                                                                                                                                                                                                                                                                               Shirasu Y., Yoshida H., Matsuki S., Takemura K., Ikeda N.,
Shimada Y., Ozawa T., Mikayama T., Iljima H., Ishida A., Sato Y.,
Tamai Y., Tanaka J., Ikenaga H.;
                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                           Tamal Y., Tanaka J., Ikenaga H.; "Molecular cloning and expression in Escherichia coli of a cDNA encoding human pancreatic elastase 2."; J. Blochem. 102:1555-1563(1987).
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V -> K (IN REF. 2).
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BAC6FE69AF4DDE56 CRC64;
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L -> S (IN REF. 2
N -> K (IN REF. 2
                       01 AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
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SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00144; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
Hydrolase; Serine protease; Zymogen; Signal.
 269 AA.
                                                                                                                                                                                                                                                                                                                                                                                                               and Phe-1-Xaa. Hydrolyzes elastin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Interpro; IPR001314; Chymotrypsin.
Interpro; IPR001254; Ser_protease_Try.
Pfam; PF00089; trypsin; 1.
                                                                   Elastase 2 precursor (EC 3.4.21.71).
                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-87217962; Pubmed-3646943;
                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE-88198076; PubMed-2834346;
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EMBL; D00237; BAA00166.1; -.
PIR; A26823; A26823.
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STANDARD;
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MEROPS; S01.155;
                                                                                              Sus scrofa (Pig)
                                                                                                                                       NCBI_TaxID-9823;
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ACT_SITE
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DISULFID
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                                               6
                                                                                                                                                                                   |:| SLSTNEPGSLAVKVSKLVYHQDWNSNQLSNGNDIALLKLASPVSLTDKIQLGCLPAAGTI 148
                                                                                                                                                                                                                                       LPSGLTCVTTGWGRISGVGNVTPARLQQVVLPLVTVNQCRQ--YWGARITDAMICAGGSG 173
                                                                                                                                                                                                                                                             174 -ASSCQGDSGGPLVCQKGN-TWVLIGIVSWGTK-NCN-IQAPAMYTRVSKFSTWINQVWA 229
                                                                                                                                                                                                                                                                                                                                      208 IISSCNGDSGGPLNCQGANGQWQVHGIVSFGSSLGCNYYHKPSVFTRVSNYIDMINSVIA 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                              58 DRSSNAEPVQVLSIARAITHPNWNANTMN--NDLTLLKLASPARYTAQVSPVCLASTNEA 115
                                                 Gaps
                                                                                                          1 IVNGENAVPGSWPWQVSLQ-DNTG--FHFCGGSLISPNWVVTAAHCQVTPGRHFVVLGEY 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -i- TISSUE SPECIFICITY: PANCREAS.
-i- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. ELASTASE SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-82182967; PubMed-6918221;
McDonald R.J., Swift G.H., Quinto C., Swain W., Pictet R.L.,
Nikovites W., Rutter W.J.;
Nikovites W., Rutter W.J.;
Primary structure of two distinct rat pancreatic preproclastases
determined by sequence analysis of the complete cloned messenger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rat
                                                 12;
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       Length 269;
                                                 82; Indels
           DB 1;
40.2%; Score 503; DB 1;
44.2%; Pred. No. 5.1e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JUL-1986 (Rel. 01, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Elastase 2 precursor (EC 3.4.21.71).
                                               41; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; V01233; CAA24543.1; -.
EMBL; L00124; AAA98780.1; -.
EMBL; L00118; AAA98780.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ribonucleic acid sequences.";
Biochemistry 21:1453-1463(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequ
15-JUN-2002 (Rel. 41, Last anno
                                               Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10116;
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58 DRS--SNAEPVQVLSIARAITHPNWNANTM--NNDLFLLKLASPARYTAQVSPVCLASTN 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    114 EALPSGLTCVTTGWGRISGVGNVTPARLQQVVLPLVTVNQCRQ--YWGARITDAMICAGG 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              172 SGASSCQGDSGGPLVCQKGN-TWVLIGIVSW-GTKNCN-1QAPAMYTRVSKFSTWINQVM 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72 DRSVLEGSEQVIPINAGDLFVHPLWNSNCVACGNDIALVKLSRSAQLGDKVQLANLPPAG 131
"Autolysis of proproteinase E in bovine procarboxypeptidase A ternary complex gives rise to subunit III."; FEBS Lett. 277:37-41(1990).
                                                                                                                                                                                                                                                                                                  A TAIL CAISALLOCARATH (1.7) AND A TAIL CAISALLOCARATH (1.7) A TAIL CAISALL STRUCTURE OF DOVING PROCESSE A TOWCTION DEFECTIVE ELASTASE-LIKE SERINE PROTEASE. DOES NOT SEEM TO HAVE A PROTEASE A AGAINST DENATURATION IN THE ACIDIC PROCARBOXYPEPTIDASE A AGAINST DENATURATION IN THE ACIDIC PROCARBOXYPERTIDASE A GRING DODENUM.

-I. SUBBUNIT: HETEROTRIMER OF SUBBUNIT III; CARBOXYPEPTIDASE A AND CHYMOTRYPSINGEN C.
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                                                                                                                                          P., Laurent G.;
subunit III, a
pancreatic 6 S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               reas; Digestion; 3D-structure.
ACTIVATION PEPTIDE.
PROPROTEINASE E.
                                                                                                                                                                                     defective endopeptidase present in the bovine pancreatic procarboxypeptidase A complex."; Eur. J. Biochem. 157:91-99(1986).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  _{\rm S1}
                                                                                            SEQUENCE OF 14-253, AND DISULFIDE BONDS.
MEDLINE=86220198; PubMed=3519215;
Venot N. Sciaky M., Puigserver A., Desnuelle
"Amino acid sequence and disulfide bridges of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SUBCELLULAR LOCATION: Extracellular.
-!- TISSUE SPECIFICITY: PANCREAS.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Interpro; IPR001314; Chymotrypsin.
Interpro; IPR001254; Ser_protease_Try.
Pfam; PF00089; trypsin; 1.
PRNTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_DOM; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
Serine protease homolog; Pancreas, Digest
PROPEP
                                                                                                                                                                                                                                                                                      X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).
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103
206
187
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PDB; 1FON; 14-OCT-96.
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171
196
253 AA;
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Matches 106;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    116 LPSGLTCVTTGWGRISGVGNVTPARLQQVVLPLVTVNQC--RQYWGARITDAMICAGGSG 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                151 LPNNYPCYVTGWGRLQTNG-ATPDVLQQGRLLVVDYATCSSASWWGSSVKTNMVCAGGDG 209
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15-DEC-1998 (Rel. 37, Last sequence update)
15-UN-2002 (Rel. 41, Last sequence update)
111) (Procarboxypeptidase A-S6 subunit III) (PROCPA-S6 III).
111) (Procarboxypeptidase A-S6 subunit III) (PROCPA-S6 III).
112) (Association of the process of the pr
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SIMILARITY).
SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12;
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MEDLINE-91099520; PubMed-2269366;
Pascual R., Vendrell J., Aviles F.X., Bonicel J., Wicker C.,
Puigserver A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 271;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89; Indels
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| 125C783B857B71E3 CRC64;
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(BY
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CHARGE RELAY SYSTEM
CHARGE RELAY SYSTEM
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                                                                                                                                                                                                                                                                                                                                                                           Hydrolase; Serine protease; Zymogen; Signal.
SIGNAL 1 16
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37; Mismatches
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                                                                                                                                                                                            InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00089; trypsin; I.
PRINTS; PR00722; CHYMOTRPEIN.
SMART; SM0020; Tryp_SPC; I.
PROSITE; PS50240; TRYPSIN_DOM; I.
PROSITE; PS00134; TRYPSIN_HIS; I.
PROSITE; PS00135; TRYPSIN_BER; I.
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                                 L00120; AAA98780.1; J
L00121; AAA98780.1; J
L00122; AAA98780.1; J
L00123; AAA98780.1; J
            AAA98780.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 104; Conservative
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Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   214
271 AA;
                                                                                                                           PIR; A00961; ELRT2.
HSSP; P00772; 1ELG.
MEROPS; S01.155; -.
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P05805;
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ACT_SITE
ACT_SITE
DISULFID
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Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: ACTS UPON ELSTIN.
-!- CATALYTIC ACTIVITY: Preferential cleavage: Leu-|-Xaa, Met-|-Xaa and Phe-|-Xaa. Hydrolyzes elastin.
-!- SUBCELLUAR LOCATION: Secreted.
-!- SUBCELLUAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: PANCREAS.
-!- TISSUE SPECIFICITY: BELONGS TO PEPTIDASE FAMILY S1. ELASTASE SUBFAMILY.
                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-87217962; PubMed-3646943;
Kawashima I., Tani T., Shimoda K., Takiguchi Y.;
Characterization of pancreatic elastase II cDNAs: two elastase II
mRNAs are expressed in human pancreas.";
DNA 6:163-172(1987).
                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Pancreas;
MEDLINE-88198076; PubMed-2834346;
Shirasu Y., Yoshida H., Matsuki S., Takemura K., Ikeda N., Shima Ozawa T., Mikayama T., Iljima H., Ishida A., Sato Y., Tamai Y., Tanaka J., Ikenaga H.;
Tanaka J., Ikenaga H.;
"Moleoular cloning and expression in Escherichia coli of a cDNA encoding human phareatic elastase 2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fletcher T.S., Shen W.F., Largman C.; "Primary structure of human pancreatic elastase 2 determined by sequence analysis of the cloned mRNA."; Biochemistry 26:7256-7261(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                           01-AUG-1988 (Rel. 08, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Elastase 2A precursor (EC 3.4.21.71).
                                                               269 AA
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InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00089; trypsin; 1.
                                                               PRT;
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SEQUENCE FROM N.A.
MEDLINE-88107669; PubMed-3427074;
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                                                                                                      08, Created)
08, Last sequ
                                                                                                                                                                                                                    Chordata;
Primates;
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                                                               STANDARD;
                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                  Homo sapiens (Human)
                                                        EL2A_HUMAN STANI
P08217; Q14243;
O1-AUG-1988 (Rel. 0:
01-AUG-1988 (Rel. 0:
15-JUN-2002 (Rel. 4
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                                       EL2A_HUMAN
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                  RESULT 12
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229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  208 VISSCNGDSGGPLNCQASDGRWQVHGIVSFGSRLGCNYYHKPSVFTRVSNYIDWINSVIA 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 IVNGENAVPGSWPWQVSLQDNTG---FHFCGGSLISPNWVVTAAHCQVTPGRHFVVLGEY 57
                                                                                                                                                                                         BY SIMILARITY.
BY SIMILARITY.
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CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                174 A-SSCQGDSGGPLVCQKGN-TWVLIGIVSWGTK-NCN-IQAPAMYTRVSKFSTWINQVMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       116 LPSGLTCVTTGWGRISGVGNVTPARLQQVVLPLVTVNQCRQ--YWGARITDAMICAGGSG
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Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               12;
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MEDLINE-88087253; PubMed-2826474;
Tani T., Ohsumi J., Mita K., Takiguchi Y.;
Tani T., Ohsumi J., Mita R., Takiguchi Y.;
"Identification of a novel class of elastase isozyme, human pancreatic elastase III, by cDNA and genomic gene cloning.";
J. Biol. Chem. 263:1231-1239(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                 Length 269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               85; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
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15-JUN-2002 (Rel. 41, Last annotation update)
Elastase IIIB precursor (EC 3.4.21.70) (Protease E).
ELA3B.
                                                                                                                                                ACTIVATION PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                 Score 486; DB 1;
Pred. No. 1.7e-36;
                SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
Hydrolase; Serine protease; Zymogen; Signal.
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                                                                                                                                                                       ELASTASE
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16-OCT-2001 (Rel. 40, Last segu
15-JUN-2002 (Rel. 41, Last anno
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
PRINTS; PR00722; CHYMOTRYPSIN
                                                                                                                                                                                                                                                                                                                                                                          28888 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 104; Conservative
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                                                                                                                                                                                                                                                                                                                                                                        269 AA;
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ID EL3B_HUMAN
AC P08861; P11423;
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DISULFID
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ACT_SITE
ACT_SITE
CONFLICT
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CONFLICT
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EL2_BOVIN
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                                                                                                                                                                                                                                                                                                                                        the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                              between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                         Wendorf P., Geyer R., Sziegoleit A., Linder D.; Localization and characterization of the glycosylation site of human
                                                                                                                                                                                                                                                                                  -!- SİMILARITY: BELONGS TO PEPTIDASE FAMILY S1. ELASTASE SUBFAMILY.
                                                                                                                                                                                                                                      -!- FUNCTION: EFFICIENT PROTESSE WITH ALANINE SPECIFICITY BUT ONLY LITTLE ELASTOLYTIC ACTIVITY.
-!- CATALYTIC ACTIVITY: Preferential cleavage: Ala-|-Xaa. Does not hydrolyse elastin.
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CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
BY SIMILARITY.
PROBABLE.
MEDLINE-88000545; PubMed-3477287;
Shen W., Fletcher T.S., Largman C.;
"Primary structure of human pancreatic protease E determined by
sequence analysis of the cloned mRNA.";
Biochemistry 26:3447-3452(1987).
                                                                                       MEDLINE-89325560; PubMed-2753124;
Moulard M., Kerfelec B., Mallet B., Chapus C.;
"Identification of a procarboxypeptidase A-truncated protease binary complex in human pancreatic juice.";
FEBS Lett. 250:166-170(1989).
                                                                                                                                                                                                                                                                                              -1- CAUTION: Was originally (Ref.5) thought to be elastase 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protease; Zymogen; Signal; Glycoprotein.
15 OR 16 (POTENTIAL).
28 ACTIVATION PEPTIDE (POTENTIAL).
                                                                                                                                                           SEQUENCE OF 94-164, AND CARBOHYDRATE-LINKAGE SITES ASN-114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-LINKED (GLCNAC. . .).
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G (IN REF. 3).
R (IN REF. 1).
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R -> G (IN REF. 3
A -> G (IN REF. 3
W -> R (IN REF. 1
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InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00089; trypsin; 1.
                                                                                                                                                                       TISSUE=Pancreas;
MEDLINE-89289996; Pubmed-2737288;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIMIS; PRO0722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS50240, TRYPSIN_DOM; 1.
PROSITE; PS00114; TRYPSIN_HIS; 1.
PROSITE; PS001135; TRYPSIN_HIS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BY
BY
BY
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                                                                                                                                                                                                                  pancreatic elastase 1.";
FEBS Lett. 249:275-278(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                      BC005216; AAH05216.1;
M18692; AAA58454.1; -.
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64
79
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PIR; A27206; A27206.
PIR; S04999; S04999.
PIR; S04490; S04490.
HSSP; P05805; IFON.
MEROPS; S01.205; -.
                                                                  SEQUENCE OF 31-50.
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                                                                               TISSUE-Pancreas;
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CHAIN
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SGASSCQGDSGGPLVC-QKGNTWVLIGIVSW-GTKNCNI-QAPAMYTRVSKFSTWINQVM 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DRSSNAEPVQVLSI--ARAITHPNWNANTM--NNDLTLLKLASPARYTAQVSPVCLASTN 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         114 EALPSGLTCVTTGWGRISGVGNVTPARLQQVVLPLVTVNQCRQ--YWGARITDAMICAGG 171
                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                            1 IVNGENAVPGSWPWQVSLQ-DNTG--FHFCGGSLISPNWVVTAAHCQVTPGRHFVVLGEY 57
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13;
                                                                                                                                                                                                   38.5%; Score 481.5; DB 1; Length 270; 42.7%; Pred. No. 4.3e-36; Live 39; Mismatches 86; Indels 13
                                                    164 R -> P (IN REF. 3).
29293 MW; B14BE0AAD3695AFE CRC64;
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15-JUN-2002 (Rel. 41, Last annotation update)
Elastase 2 precursor (EC 3.4.21.71).
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InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00089; trypsin; 1.
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MEDLINE=98079203; PubMed=9418008;
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01-NOV-1997 (Rel. 35, Last sequ
15-JUN-2002 (Rel. 41, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X97635; CAA66231.1; -. HSSP; P00766; 1CHG.
                                                                                                                                                                                                                                                                                                        Matches 103; Conservative
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NCBI_TaxID=9913;
                                                                                                    270 AA;
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                       174 -ASSCOGDSGGPLVCQKGN-TWVLIGIVSWGTK-NCN-IQAPAMYTRVSKFSTWINQVMA 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       208 VTSSCNGDSGGPLNCQAANRQWQVHGIVSFGSSLGCNYYRKPSVFTRVSNYNDWISSVIE 267
                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                              29 VVGGEDARPNSWPWQVSLQYSSSGQWRHTCGGSLIEQNWVLTAAHCISSSRTXRVVVGRQ 88
                                                                                                                                                                                                                                                                                                                               1 IVNGENAVPGSWPWQVSLQDNTG---FHFCGGSLISPNWVVTAAHCQVTPGRHFVVLGEY 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and Phe-|-Xaa. Hydrolyzes elastin.
-- SUBCELULAR LOCATION Secreted.
--- TISSUE SPECIFCITY: PANCHES.
--- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. ELASTASE SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Met-|-Xaa
PRINTS; PR00722; CHILLER SHART; SM0020; TYPESPS 1.

PROSITE; PS60240; TRYPSIN_DOM; 1.

PROSITE; PS00134; TRYPSIN_HIS; 1.

PROSITE; PS00135; TRYPSIN_ER; 1.

PROSITE; PS00135; TRYPSIN_ER; 1.

Hydrolase; Serine protease; Zymogen; Signal.

BY SIMILARITY.

ACTIVATION PEPTIDE (BY SIMILARITY).

ACTIVATION PEPTIDE (BY SIMILARITY).

ACTIVATION PEPTIDE (BY SIMILARITY).

ACTIVATION PEPTIDE (BY SIMILARITY).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                   12;
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                                                                                                                                                                                                                                                                       Length 269;
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Nucleic Acids Res. 14:8307-8330(1986).
-!- FUNCTION: ACTS UPON ELASTIN.
-!- CATALYTIC ACTIVITY: Preferential cleavage: Leu-|-Xaa,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=87066713; PubMed=3641189;
Stevenson B.J., Hagenbuechle O., Wellauer P.K.;
"Sequence organisation and transcriptional regulation of
                                                                                                                                                                                                                                                                  38.3%; Score 480; DB 1; Length 26
42.6%; Pred. No. 5.9e-36;
1ve 39; Mismatches 88; Indels
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13-AUG-1987 (Rel. 05, Last sequence update)
13-UUN-2002 (Rel. 41, Last annotation update)
Elastase 2 precursor (EC 3.4.21.71).
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216
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269 AA;
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P05208;
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                                                                                                                                                                                                                                                                                         SIMILARITY).
SIMILARITY).
SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  174 -ASSCOGDSGGPLVCOKGN-TWVLIGIVSWGTK-NCNI-QAPAMYTRVSKFSTWINQVMA
                                                                                                                                                                                                                                                                                                                                                                                                                            12;
                                                                                                                                                                                                                                                                                                                                                                                                 Score 475; DB 1; Length 271;
Pred. No. 1.7e-35;
9; Mismatches 93; Indels
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                                                                EMBL, X04573; CAA28242.1; --
EMBL, X04576; CAA28244.1; --
PIR; A25528; A25528.
HSSP, P00772; 1ELG.
MENOPS; S01.155; --
MGD; MGI.95316; Ela2.
InterPro; 1PR001314; Chymotrypsin.
InterPro; 1PR001354; Ser_Protease_Try.
Pfam; PR00089; trypsin, 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMARY; SM00020; Tryps_SPC; 1.
PROSITE; PS5040; TRYPSIN. JOM; 1.
PROSITE; PS00134; TRYPSIN. HS; 1.
PROSITE; PS00135; TRYPSIN. HS; 1.
PROSITE; PS00135; TRYPSIN. SER; 1.
PHOGOIRS; Sofine protease; Zymogen; Signal.
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tive 39; Mismatches
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Job time: 8.91304 secs
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GenCore version 5.1.3

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OM protein - protein search, using sw model

Run on: December 20, 2002, 15:14:28; Search time 14.6087 Seconds

(without alignments)
1520.126 Million cell updates/sec

Title:
US-09-856-3198-4_COPY_34_264

Perfect score: 1252
Sequence: 1 17NGENAVPGSWPWOVSLQD......AMYTRVSKFSTWINQVMAYN 231

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 1008
Listing first 45 summaries

Listing first 45 summaries

Database: PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ES	Description	chymotrypsin-like	٠ -	EC DE	) EC	S S	EC.		В	pancreatic elastas	elŝ	polyprotein - Afri	pancreatic elastas	procarboxypeptidas	pancreatic elastas	pancreatic elastas	7)	plasmin (EC 3.4.21	pancreatic elastas	1 trypt	plasmin (EC 3.4.21	(EC 3.4	(EC 3.4	ic elas		pancreatic elastas	pancreatic elastas	tryptase (EC 3.4.2	4	chymotrypsin-like
SUMMARIES	ID		A21195	S47537	A31299	KYBOB	KYBOA	KYRTB	872219	A26823	ELRT2	T30337	B26823	CPBOA3	B29934	A25528	PLHU	PLMS	A29934	S56160	B61545	B30848	PLPG	C26823	A57014	S68826	S68825	A47246	כי	A23473
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	Length	264	263	263	. 263	245	245	263	244	269	271	1524	269	240	270	271	810	812	270									273	231	126
đ	Query Match	89.4	60.5	59.9	59.9	59.1	58.1	57.1	57.1	40.2	39.9	38.9	38.8	38.8	38.5	37.9	37.1	36.9	36.8	36.4	36.1	36.1	35.9	35.9	35.8	35.7	35.7	35.7	35.5	35.2
	Score	1119	757.5	750.5	750.5	740.5	727.5	715.5	714.5	503	499	487	486	485.5	481.5	7	464.5	o	460.5	455.5	52.	451.5	449.5	4	448.5	447.5	47.	447.5	444	441
	Result No.	7	7	en	4	'n	9	7	80	6	10	11	12	13	14	15	16	17	.18	19	50	21	22	23	24	25	56	27	28	29

RESULT 2
A21195
chymotrypsin (EC 3.4.21.1) 2 precursor - dog
cyprocies: Canis lupus familiaris (dog)
C;Species: 27-ul-1990 #sequence_revision 27-Jul-1990 #text_change 22-Jun-1999
C;Accession: A21195

9 9 à g

tryptase (EC 3.4.21 tryptase (EC 34.2 plannin (EC 3.4.21) trypsin (EC 3.4.21) pancreatic elastas maxi Cell proteina trypsin (EC 3.4.21) enteropeptidase (EC 3.4.21) enteropeptidase (EC 3.4.21) pancreatic elastas probable pancreati tryptase (EC 3.4.21) pancreatic elastas probable pancreati tryptase (EC 3.4.21)	RESULT 1 138.16 chymotrypsin-like proteinase (EC 3.4.21) CTRL-1 - human C;Species: Homo sapiens (man) C;Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 22-Jun-1999 C;Accession: 138136 R;Larsen, F.; Solhelm, J.; Kristensen, T.; Kolsto, A.B.; Prydz, H. Hum. Mol. Genet. 2, 1589-1595, 1993 A;Title: A tight cluster of five unrelated human genes on chromosome 16q22.1. A;Reference number: 138135; MUD:94093544; PMID:8268911 A;Accession: 138136 A;Accessio	tch  89.4%; Score 1119; DB 2; Length 264;  al Similarity 86.1%; Pred. No. 6.2e-90;  1999; Conservative 22; Mismatches 10; Indels 0; Gaps 0;  IVNGENAVDGSWPWQVSLQDNTGFHFCGGSLISPNWVVTAAHCQVTPGRHFVVLGEYDRS 60
TRRT1 A6171 A61845 TRRT2 TRDGC TRDGC S55067 ELRT1 A38654 A38618 A56118 A5615 C35863	ALIGNMENT  C 3.4.21) CT  evision 06-Sep  tensen, T.; Ko 1933 e unrelated hu b:94093544; bw ed from GB/EMB ed from GB/EMB  for 167/1; 21 homology roteinase gy <try> ASP, Ser #stat</try>	## SCOTE 1119  ## SCO
22 4 4 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	mase (E (man)   quence_r   fuence_r   fuence_r   fuence_r   fuence_r   fuence_r   fuence_r   fuence_r   fuence_r   fuence_r   fuence   f	89.4%; 86.1%; vative "QVSLQDNTC        :: AQVSLQDSSC AITHPNWNAI
0.00.00.00.00.00.00.00.00.00.00.00.00.0	e protes sapiens 136 11.56 2, 158 2, 158 136 1136 1136 1137; 1136 1137; 1136 1136 1136 1136 1136 1136 1136 113	Similarity 86. Similarity 86. 99. Conservative (GENAVPGSWPWQVSLQ
439.5 430.5 436.4 433.6 433.6 430.5 420.5 420.5 420.5 420.5 420.5 420.5 420.5 420.5 420.5	Ppsin-lik 98: Homo 106-Sep-1 106-Sep-1 107-Sep-1 107-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 108-Sep-1 1	/ Match Local Simile nes 199; Cc 1 IVNGENAVE 34 IVNGENAVI                                 94 SNAEPLOVI
W W W W W W W W W W W W W W W W W W W	RESULT 138136 chymotry C; Spacts: C; Date: C; Date: C; Date: C; Date: A; Refere: A; Refere: A; Residu A; R	Query Match Best Local Matches 19 Qy 1 IVW Db 34 IVW QY 61 SNA Db 94 SNA

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Query Match
                       213
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R;Pinsky, S.D.; LaForge, K.S.; Luc, V.; Scheele, G.
Proc. Natl. Acad. Sci. U.S.A. 80, 7486-7490, 1983
A;Title: Identification of cDNA clones encoding secretory isoenzyme forms: sequence dete
A;Reference number: A21195; MUID:84170253; PMID:6584866
A;Accession: A21195
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C;Species: Gadus morhua (Atlantic cod)
C;Date: 26-Dec-1994 **Requence_revision 03-Aug-1995 **text_change 22-Jun-1999
C;Accession: S47537; S43163
R;Gudmundsdottir, A.; Oskarsson, S.; Eakin, A.E.; Craik, C.S.; Bjarnason, J.B.
Biochim. Biophys. Acta 1219, 211-214, 1994
A;Title: Atlantic cod cDNA encoding a psychrophilic chymotrypsinogen.
A;Reference number: S47537; MUID:94368860; PMID:8086467
A;Accession: S47537.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A Molecule type: mRNA
A; Residues: 1-263 <GUD>
A; Cross-references: EMBL: X78490; NID:q468750; PIDN:CAA55242.1; PID:q468751
C; Superfamily: trypsin; trypsin homology
C; Keywords: hydrolase; protein digestion; serine proteinase
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-263/Product: chymotrypsin #status predicted <MAT>
F;34-256/Domain: trypsin homology <TRX>
F;75,120,213/Active site: His, Asp, Ser #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93 SNSEGVOVMTVGQVFKHPRYNGFTINNDILLVKLATPATLNMRVSPVCLAETDDVFEGGM 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            153 LCVTTGWGLTKHTNANTPDKLQQAALPLLSNAECKKFWGSKITDLMVCAGASGVSSCMGD 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SNAEPVQVLSIARAITHPNWNANTMNNDLTLLKLASPARYTAQVSPVCLASTNEALPSGL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 TCVTTGWGRISGVGNVTPARLQQVVLPLVTVNQCRQYWGARITDAMICAGGSGASSCQGD 180
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                                                                                                                                                                                     PID:9163946
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                                                                                                                                                                                                                                                                                                                      60.5%; Score 757.5; DB 2; Length 263; 58.0%; Pred. No. 1.7e-58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SGGPLVCQKGNTWVLIGIVSWGTKNCNIQAPAMYTRVSKFSTWINQVMAYN 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SGGPLVCQKGNTWVLIGIVSWGTKNCNIQAPAMYTRVSKFSTWINQVMAYN
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                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-263 <PIN>
A; Cross-references: GB:KO173; NID:g163945; PIDN:AAA30841.1;
C; Superfamily: trypsin; trypsin homology
C; Keywords: hydrolase; protein digestion; serine proteinase
F; 34-256/Domain: trypsin homology <TRY>
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F;75,120,213/Active site: His, Asp, Ser #status predicted
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                                                                                                                                                                                                                                                                                                                                                                        35; Mismatches
                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 58.0
Matches 134; Conservative
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C; Accession: A00953
R; Smillie, L.B.; Furka, A.; Nagabhushan, N.; Stevenson, K.J.; Parkes, C.O.
R; Smillie, L.B.; Furka, A.; Nagabhushan, N.; Stevenson, K.J.; Parkes, C.O.
R; Smillie, L.B.; Furka, A.; Nagabhushan, N.; Stevenson, K.J.; Parkes, C.O.
R; Smillie, L.B.; Furka, M.D.; Stevenson, K.J.; Parkes, C.O.
R; Title: Structure of fokymotrypsinogen B compared with chymotrypsinogen A and trypsin
A; Reference number: A00953; MUD: 68238908; PMID: 5649671
A; Residues: 1-245 SMID
A; Residues: 1-245 SMID
A; Residues: 1-245 SMID
C; Comment: The first activation cleavage, leading to pi-chymotrypsinogen A, in the a C; Comment: The first activation cleavage, leading to pi-chymotrypsin B, occurs in the C; Superfamily: trypsin; trypsin homology
C; Keywords: Hydrolase; pancreas; protein digestion; serine proteinase; zymogen
F; 1-15/Domain: propeptide #status experimental <AMI>F; 16-245/Product: chymotrypsin B #status experimental <AMI>F; 11-22, 42-58 J36-201, 168-182, 191-220/Disulfide bonds: #status experimental
F; 57,102,195/Active site: His, Asp, Ser #status experimental
                                                                                                                                                                                                                                                                                                                                          R;Tomita, N.; Izumoto, Y.; Horii, A.; Doi, S.; Yokouchi, H.; Ogawa, M.; Mori, T.; Mat Biochem. Biophys. Res. Commun. 158, 569-575, 1889
A;Title: Molecular cloning and nucleotide sequence of human pancreatic prechymotrypsi A;Reference number: A31299; MUID:89134264; PMID:2917002
A;Accession: A31299
A;Molecular prainfinary
A;Molecule type: mRNA
A;Residues: 1-263 <TOM>
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C;Species: Bos primigenius taurus (cattle)
C;Date: 08-Oct-1981 #sequence_revision 08-Oct-1981 #text_change 18-Jul-1997
                                                                                                                                                                                                                                                     Species: Homo sapiens (man)
:Date: 08-Jun-1989 #sequence_revision 08-Jun-1989 #text_change 22-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SNAEPVQVLSIARAITHPNWNANTMNNDLTLLKLASPARYTAQVSPVCLASTNEALPSGL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references: GB:M24400; NID:9181189; PIDN:AAA52128.1; PID:9181190
C; Genetics:
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Length
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C;Keywords: hydrolase; protein digestion; serine proteinase
F;34-256/Domain: trypsin homology <TRY>
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larity 58.0%; Pred. No. 6.9e-58;
Conservative 35; Mismatches 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chymotrypsin (EC 3.4.21.1) B precursor - bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OMIM:118890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GDB:119820; OMIM:1188
A;Map position: 16q23.1-16q23.1
C;Superfamily: trypsin; trypsin homology
                                                                                                                                                                                                                       chymotrypsin (EC 3.4.21.1) precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 134; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Gene: GDB:CTRB1; CTRB
                                                                                                                                                                                                                                                                                                                           Accession: A31299
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F;16-238/Domain: trypsin homology <TRY>
F;1-122,42-58,136-201,168-182,191-220/Disulfide bonds: #status
F;57,102,195/Active site: His, Asp, Ser #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 55.49
Matches 128; Conservative
                                                                                                                                 Query Match
Best Local Similarity
Matches 131; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A Accession: A22658
A Molecule type: DNA
A Residues: 1-263 <BEL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chymotrypsin (EC 3.4.21.1) A precursor - bovine
N; Alternate names: chymotrypsinogen A
C; Species: Bos primigenius taurus (cattle)
C; Species: Bos primigenius taurus (cattle)
C; Species: 07-May-1981 #sequence_revision 07-May-1981 #text_change 07-May-1999
C; Accession: A90235; A93158; S29650; A00952
R; Brown, J.R.; Hartley, B.S.
Biochem, J. 101, 214-228, 1966
A; Title: Location of disulphide bridges by diagonal paper electrophoresis. The disulphid A; Reference number: A90235; MUID:67181721; PMID:5971783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: protein
A; Mealdues: 1-101, N', 103-245 < MEL>
A; Realdues: 1-101, N', 103-245 < MEL>
A; Realdues: 1-101, N', 103-245 < MEL>
A; Mote: disulfide bonds were determined
B; Curruzzola, F.; Ascenzi, P.; Barra, D.; Bolognesi, M.; Menegatti, E.; Sarti, P.; Schne
Biochim. Biophys. Acta 1161, 201-208, 1993
Biochim. Biophys. Acta 1161, 201-208, 1993
A; Title: Selective oxidation of Met-192 in bovine alpha-chymotrypsin. Effect on catalyti
A; Reference number: S29650; MUID:93160238; PMID:8431470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.; Vanacek, J.; Keil, B.; Sorm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Wolecule type: protein

R; Residues: 1-101, N', 103-245 <BRO>
R; Residues: 1-101, N', 103-245 <BRO>
R; Residues: 1-101, N', 103-245 <BRO>
R; Blow, D.M.; Birktoft, J.J.; Hartley, B.S.
Nature 221, 337-340, 1969

A; Title: Role of a buried acid group in the mechanism of action of chymotrypsin. A; Reference number: A93158; MulD: 69106266; PMID: 5764436

A; Reference annotation; revision to residue 102

R; Meloun, B.; Kluh, I.; Kostka, V.; Moravek, L.; Prusik, Z.; Vanacek, J.; Keil, i Bochim. Blophys. Acta 130, 543-546, 1966

A; Title: Covalent structure of bovine chymotrypsinogen A.

A; Reference number: A90572; MUID: 67183948; PMID: 5972866

A; Accession: A93158
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A; Residues: 1-12:16-27;149-160;181-200 <CUT>
R; Smillie, L.B; Hartley B.S.
Blochem. J. 101, 232-241, 1966
A; Title: Histidine sequences in the active centres of some 'serine' proteinases.
A; Reference number: A90236; MUID:67181723; PMID:5971785
A; Contents: annotation; active site
R; Birktoft, J.J; Blow, D.M; Henderson, R.; Steitz, T.A.
Philos. Trans. R. Soc. Lond. B257, 67-76, 1970
                                                                     ij
                                                                                                                                                                                                                                                         61 SNAEPVQVLSIARAITHPNWNANTMNNDLTLLKLASPARYTAQVSPVCLASTNEALPSGL 120
                                                                                                                                                                                                                                                                                              TCVTTGWGRISGVGNVTPARLQQVVLPLVTVNQCRQYWGARITDAMICAGGSGASSCQGD 180
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                                                                                                                           1 IVNGENAVPGSWPWQVSLQDNTGFHFCGGSLISPNWVVTAAHCQVTPGRHFVVLGEYDRS 60
                                                                                                                                                            16 IVNGEDAVPGSWPWQVSLQDSTGFHFCGGSLISEDWVVTAAHCGVTTS-DVVVAGEFDQG 74
                                                                     ï
      Length 245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              195 SGGPLVCQKNGAWTLAGIVSWGSSTCSTSTPAVYARVTALMPWVQETLAAN 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGGPLVCQKGNTWVLIGIVSWGTKNCNIQAPAMYTRVSKFSTWINQVMAYN 231
                                                                  Indels
   DB 1;
                                 Pred. No. 4.7e-57
                                                               32; Mismatches
   59.1%; Score 740.5; 57.1%; Pred. No. 4.7
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                             Best Local Similarity 57.19
Matches 132; Conservative
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N;Alternate names: chymotrypsinogen B
C;Species: Rattus norvegicus (Norway rat)
C;Species: Battus norvegicus (Norway rat)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 18-Jun-1999
C;Accession: A22658
R;Bell, G.L.; Quinto, C.; Quiroga, M.; Valenzuela, P.; Craik, C.S.; Rutter, A;Diol. Chem. 259, 14265-14270, 1984
A;Title: Isolation and sequence of a rat chymotrypsin B gene.
A;Reference number: A22658; MUID:85054881; PMID:6209274
experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 SNAEPVQVLSIARAITHPNWNANTMNNDLTLLKLASPARYTAQVSPVCLASTNEALPSGL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 TCVTTGWGRISGVGNVTPARLQQVVLPLVTVNQCRQYWGARITDAMICAGGSGASSCQGD 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74
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                                                                                                                                                                                                                                                                                                                                                                                                                1 IVNGENAVPGSWPWQVSLQDNTGFHFCGGSLISPNWVVTAAHCQVTPGRHFVVLGEYDRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16 IVINGEBAVPGSWPWQVSLQDKTGFHFCGGSLINENWVVTAAHCGVTTS-DVVVAGEFDQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 IVNGENAVPGSWPWQVSLQDNTGFHFCGGSLISPNWVVTAAHCQVTPGRHFVVLGEYDRS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SGGPLVCQKGNTWVLIGIVSWGTKNCNIQAPAMYTRVSKFSTWINQVMAYN 231
                                                                                                                                                                                                                                                                                            , 19
                                                                                                                                                                         DB 1;
                                                                                                                                                             58.1%; Score 727.5; DB 1
ilarity 56.7%; Pred. No. 6.4e-56;
Conservative 32; Mismatches 67
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W.; Ru

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C;Accession: T30337
R;Yang, J.C.; Lindsay, L.L.; Hedrick, J.L.
R;Description: cDNA cloning of ovochymase, a chymotrypsin-like protease released from A;Reference number: 220829
R;Reference number: 220829
R;Accession: T30337
R;Cression: T303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cyaccession: A00961:
RymacDonald, R.J.; Swift, G.H.; Quinto, C.; Swain, W.; Pictet, R.L.; Nikovits, W.; Ru Biochemistry 21, 1453-1463, 1982
A;Title: Primary structure of two distinct rat pancreatic preproclastases determined A;Reference number: A00960; MUID:82182967; PMID:6918221
A;Accession: A00961...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A.Molecule type: mRNA
A.Resdues: 1-271 <MAC>
A.Cross-references: GB:L00124; GB:J00731; NID:g204019; PIDN:AAA98780.1; PID:g204021
C.Superfamily: trypsin; trypsin; homology
C.Superfamily: trypsin; trypsin; bancreas; serine proteinase; zymogen
F;1-16/Domain: signal sequence #status predicted <SIG>
F;7-30/Domain: activation peptide #status predicted <APT>
F;31-271/Product: elastase II #status predicted <MPT>
F;31-274/Domain: trypsin homology <TRY>
F;31-284/Domain: trypsin homology <TRY>
F;75,123,218/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Species: Rattus norvegicus (Norway rat)
:Date: 18-Aug-1982 #sequence_revision 18-Aug-1982 #text_change 24-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Xenopus laevis (African clawed frog)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     210 VTSSCNGDSGGPLNCQASNGQWQVHGIVSFGSTLGCNYPRKPSVFTRVSNYIDMINSVIA 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DRSSNAEPVQVLSIARAITHPNWNANTMN--NDLTLLKLASPARYTAQVSPVCLASTNEA 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LPSGLTCVTTGWGRISGVGNVTPARLQQVVLPLVTVNQC--RQYWGARITDAMICAGGSG 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               174 - ASSCQGDSGGPLVCQKGN-TWVLIGIVSWG-TKNCNI-QAPAMYTRVSKFSTWINQVMA 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IVNGENAVPGSWPWQVSLQ---DNTGFHFCGGSLISPNWVVTAAHCQVTPGRHFVVLGEY 57
                                                                                                                                                                  208 IISSCNGDSGGPLNCQGANGQWQVHGIVSFGSSLGCNYYHKPSVFTRVSNYIDWINSVIA
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                                                                                                            -ASSCQGDSGGPLVCQKGN-TWVLIGIVSWGTK-NCN-IQAPAMYTRVSKFSTWINQVMA
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Pred. No. 5.3e-36;
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43.08;
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Best Local Similarity 43.0%
Matches 104; Conservative
                                                                                                                                                                                                                                                                                                 230 YN 231
                                                                                                                                                                                                                                                                                                                                                                                     NN 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         230 YN 231
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N;Alternate names: pancreatopeptidase E
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 16-Aug.1988 #sequence_revision 16-Aug-1988 #text_change 22-Jun-1999
C;Accession: A26823
R;Kawashima, I:, Tani, T.; Shimoda, K.; Takiguchi, Y.
DNA 6, 163-172, 1987
A;Title: Characterization of pancreatic elastase II cDNAs: two elastase II mRNAs are exp
A;Reference number: A90958; MUD:87217962; PMID:3646943
A;Accession: A26823
A;Molecule type: mRNA
A;Residues: 1-269 cKAW>
A;Cross-references: GB:M16651; NID:G164441; PIDN:AAA31027.1; PID:g164442
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; serline proteinase
F;11-6/Domain: propeptide #status predicted cRNO>
F;29-269/Product: elastase II #status predicted cMTP>
F;29-262/Domain: trypsin homology cTRX>
F;29-262/Domain: trypsin
                                                                                                                                                                                                         M.; Hojrup, P.
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                                                                                                                                                                                                                                                                                                 Gadus morhua
chymotrypsin B - Atlantic cod (fragments)
C;Species: Gadus morhua (Atlantic cod)
C;Species: Gadus morhua (Atlantic cod)
C;Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 07-Aug-1998
C;Accession: S7219
R;Leth-Larsen, R.; Asgeirsson, B.; Thorolfsson, M.; Norregaard-Madsen, M.; H Biochim. Blophys. Acta 1297, 49-56, 1996
A;Title: Structure of chymotrypsin variant B from Atlantic cod, Gadus morhua A;Reference number: S72219; MUID:96439045; PMID:8841380
A;Accession: S72219
A;Accession: S72219
A;Accession: Light actain Affective Code (Cadus morhua A;Reference number: Protein A;Reference (Cadus morhua A
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<u>::</u>
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55.1%; Pred. No. 8.6e-55;
ive 41; Mismatches 57;
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Matches 129; Conservative
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C. Accession: A25065
R;Venot, N.; Sciaky, M.; Puigserver, A.; Desnuelle, P.; Laurent, G.
Eur. J. Biochem. 157, 91-99, 1986
A:Title: Amino acid sequence and disulfide bridges of subunit III, a defective endope A; Reference number: A25065; MUID:86220198; PMID:3519215
A; Accession: A25065; MUID:86220198; PMID:3519215
A; Accession: A25065; MUID:86220198; PMID:3519215
A; Accession: A15065
A; Molecule type: protein
A; Residues: 1.240 cvEN>
C; Comment: This protein is found in the pancreatic juice of ruminants, where it const c; Comment: This protein is found in the pancreatic juice of ruminants, where it const c; Comment: This protein is found in the acidic environment of the ruminant duodenum. C; Superfamily: trypsin homology cTRY>
E; Superfamily: trypsin homology cTRY>
F; 1-233/Domain: trypsin homology cTRY>
F; 28-44,87-90,127-193,158-174,183-214/Disulfide bonds: #status experimental
F; 43,93,187/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             procarboxypeptidase A complex component III - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 18-Jul-1997
                                                                                                                                                                                                                                                58 DRSSNAEPVQVLSIARAITHPNWNANTMN--NDLTLLKLASPARYTAQVSPVCLASTNEA 115
                                                                                                                                                                                                                                                                                            208 VISSCNGDSGGPLNCQASDGRWQVHGIVSFGSRLGCNYYHKPSVFTRVSNYIDMINSVIA 267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 116 LPSGLTCVTTGWGRISGVGNVTPARLQQVVLPLVTVNQCRQ--YWGARITDAMICAGGSG 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 NGENAVPGSWPWQVSLQ---DNTGFHFCGGSLISPNWVVTAAHCQVTPGRHFVVLGEYDR 59
                                                                                                                                                         174 A-SSCOGDSGGPLVCOKGN-TWVLIGIVSWGTK-NCN-IQAPAMYTRVSKFSTWINQVMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 IVNGENAVPGSWPWQVSLQDNTG---FHFCGGSLISPNWVVTAAHCQVTPGRHFVVLGEY
                                                                                                                                                                                                                                                                                                                                                                                           116 LPSGLTCVTTGWGRISGVGNVTPARLQQVVLPLVTVNQCRQ--YWGARITDAMICAGGSG
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                                           Indels
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Pred. No. 6.9e-35;
Pred. No. 7.1e-35;
Mismatches 85;
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                                    41;
   43.0%;
                                        Conservative
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Best Local Similarity
       Best Local Similarity
Matches 104; Conser
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B29934
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C; Species: Homo saptens (man)
C; Species: Homo saptens (man)
C; Species: Homo saptens (man)
C; Species: Homo saptens (man)
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C; Species: Homo saptens (man)
C; Species: Homo saptens (man)
C; Species: Homo saptens (man)
C; Species: Homo saptens (man)
R; Kawashina, I.; Tani, T.; Shimoda, K.; Takiguchi, Y.
DNA 6, 163-172, 1987
A; Title: Characterization of pancreatic elastase II CDNAs: two elastase II mRNAs are exp.
A; Reference number: A90958; WUID:87217962; PMID:3646943
A; Recession: B26823
A; Molecule type: mRNA
A; Residues: 1.269 cKAWA
A; Cross-references: GB:MI6652; NID:9182057; PIDN:AAA52380.1; PID:9182058
B; Fletcher, T. S.; Shen, W.F.; Largman, C.
Biochemistry 26, 7256-7261, 1987
A; Title: Primary structure of human pancreatic elastase 2 determined by sequence analysi
A; Reference number: A27432
A; Molecule type: mRNA
A; Residues: 1.269 cKLE>
A; Molecule type: mRNA
A; Recession: A27432
A; Molecule type: mRNA
A; Reference number: A27431; NUID:9182022; PIDN:AAA52374.1; PID:9182023
B; Shirasu, Y.; Yoshida, H.; Matsuki, S.; Takemura, K.; Ikeda, N.; Shimada, Y.; Ozawa, T.
A; Title: Molecular cloning and expression in Escherichia coli of a cDNA encoding human A; Reference number: A41431; MUID:98198076; PMID:2834346
A; Molecula type: mRNA
A; Molecula type: mRNA
A; Reference number: A41431; MUID:98198076; PMID:2834346
A; Molecula type: mRNA
A; Reference number: A41431; MUID:98198076; PMID:2834346
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A; Resternce: A41431; MOLD: 0019070; FMID: 2034340
A; Recession: A41431
A; Molecule type: mRNA
A; Residues: 1-201, 'v', 203-269 <SHI>A; Residues: 1-201, 'v', 203-269 <SHI>A; Residues: 1-201, 'v', 203-269 <SHI
A; Note: the authors translated the codon GTG for residue 202 as Cys
B; Moulard, M.; Michon, T.; Kerfelec, B.; Chapus, C.
FEBS Lett. 261, 199-183, 1990
A; Title: Further studies on the human pancreatic binary complexes involving procarboxype
A; Reference number: 508253; MUID: 90169111; PMID: 2307232
A; Recession: 534491
A; Molecule type: protein
A; Residues: 'X', 18-50 <MOU>
C; Genetics:
A; Residues: 'X', 18-50 <MOU>
C; Genetics:
A; Cross-references: GDB: 119866; OMIM: 130120
A; Cross-references: GDB: 119866; OMIM: 130120
A; Cross-references: hydrolase; pancreas; serine proteinase
C; Reywords: hydrolase; pancreas; serine prodicted <ROO>
F; 1-1-67 Domain: trypsin trypsin homology <FRV>
F; 29-269 / Product: pancreatic elastase IIA #status predicted <MAT>
F; 29-262 / Domain: trypsin homology <FRV>
FYVELED STATUS F; 201-2010 / Domain: trypsin homology <FRV>
F; 29-262 / Domain: trypsin homology <FRV>
F; 
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                                                                                                                                                                                                                       --SNAEPVQVLSIARAITHPNWNANTMNNDLTLLKLASPARYTAQVSPVCLASTNEALPS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                         GLT------CVTTGWGRISGVGNVT-PARLQQVVLPLVTVNQCRQYWGARITDAMICAG 170
                                                                                                                                                                           1 IVNGENAVPGSWPWQVSLQDNTGFHFCGGSLISPNWVVTAAHCQVTPGRHFVVLGEYDRS 60
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                                        Length 1524;
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                                ; Score 487; DB 2;
; Pred. No. 4.2e-34;
49; Mismatches 75;
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                                    38.9%;
39.5%;
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                                                                        Similarity
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Arginia: Sequence organisation and transcriptional regulation of the mouse elastase I A; Reference number: A93646; MUID:87066713; PMID:3641189
A; Reference number: A93646; MUID:87066713; PMID:3641189
A; Anolecule type: mRNA
A; Residues: 1-271 <STE>
A; Cross references: GB:X04573; NID:950825; PIDN:CAA28242.1; PID:950826
A; Cross references: GB:X04573; NID:950825; PIDN:CAA28242.1; PID:950826
C; Superfamily: trypsin; trypsin homology
C; Keywords: hydrolase; serine proteinase
F;1-30/Domain: signal sequence #status predicted <SIG>
F;31-27/Product: pancreatic elastases II #status predicted <MAT>
F;31-284/Domain: trypsin homology <FRXP
F;31-284/Domain: trypsin homology <FRXP
F;31-284/Domain: Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pancreatic elastase II (EC 3.4.21.71) precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 22-Jun-1999
C;Accession: A25528
R;Stevenson, B.J.; Hagenbuechle, O.; Wellauer, P.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 210 VTSSCNGDSGGPLNCRASNGQWQVHGIVSFGSSLGCNYPRKPSVFTRVSNYIDWINSVMA 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58 DRSSNAEPVQVLSIARAITHPNWNANTMNN--DLTLLKLASPARYTAQVSPVCLASTNEA 115
                    DRSSNAEPVQVLSI--ARAITHPNWNANTM--NNDLTLLKLASPARYTAQVSPVCLASTN 113
                                                                                                                                                                                                                                                                               SGASSCQGDSGGPLVC-QKGNTWVLIGIVSW-GTKNCNI-QAPAMYTRVSKFSTWINQVM 228
                                                                                                                                                                                                                                                                                                                     1 IVNGENAVPGSWPWQVSLQ---DNTGFHFCGGSLISPNWVVTAAHCQVTPGRHFVVLGEY 57
                                                                                                                                                                                    174 - ASSCOGDSGGPLVCQKGN-TWVLIGIVSWGTK-NCNI-QAPAMYTRVSKFSTWINQVWA
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                                                      EALPSGLTCVTTGWGRISGVGNVTPARLQQVVLPLVTVNQCRQ.--YWGARITDAMICAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 37.9%; Score 475; DB 2; L
Local Similarity 40.5%; Pred. No. 6.5e-34;
les 98; Conservative 39; Mismatches 93;
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A; Residues: 31-50 <MOU>
R; Wendorf, P.; Geyer, R.; Sziegoleit, A.; Linder, D.
RESE Lett. 249, 275-278, 1989
A; Title: Localization and characterization of the glycosylation site of human pancreatic
A; Reference number: S04490; MUID:89289996; PMID:2737288
pancreatic elastase (EC 3.4.21.36) IIIB precursor - human
N.Alternate names: 35K glycoprotein; pancreatic protein P35; protein G32; proteinase E
C;Species: Homo sapiens (man)
C;Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 22-Jun-1999
C;Accession: B29934, A90516; A27206; A33257; A28932; S04999; S04490
C;Accession: B29934, A90516; A27206; A33257; A28932; S04999; S04490
A;Tain, T.; Ohsumi, J.; Mita, K.; Takiguchi, Y.
J. Biol. Chem. 263, 1231-1239, 1988
A;Title: Identification of a novel class of elastase isozyme, human pancreatic elastase
A;Accession: B2934
A;Accession: B2934
A;Accession: B2934
A;Residues: 1-270 cTANA
A;Residues: 1-270 cTANA
                                                                                                                                                                                                                                                                                                                                                                                                                                               Rishen, W.; Fletcher, T.S.; Largman, C.
Bochemistry 26, 3447-3452, 1987
A;Title: Primary structure of human pancreatic protease E determined by sequence analysi
A;Reference number: A90516; MUID:88000545; PMID:3477287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Mesiduces: (4',5-63', (4',5-78,'W',80-163,'P',165-270 <FLE>
R; Artlas. F.X.; Pascual, R.; Salva, M.; Bonicel, J.; Putgserver, A.
Blochem. Biophys. Res. Commun. 163, 1191-1196, 1989
A; Title: Generation of a subunit III-11ke protein by autolysis of human and porcine prog
A; Reference number: A33257; MUID:89392022; PMID:2675835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: protein
A; Residues: 18-57 <AVI>
R; Residues: 18-57 <AVI>
R; Cotte, 0.; Barthe, C.; Basso, D.; Fournet, B.; Figarella, C.
Biochem. Biophys. Res. Commun. 156, 318-322, 1988
A; Title: Characterization of two glycoproteins of human pancreatic juice: P35, a truncat A; Reference number: A28932; MUID: 89025862; PMID: 3178837
A; Accession: A28932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: protein
A; Residues: 'X',32-52,'X',54-55,'XXX',59-63 <GUY>
R; Moulard, M.; Kerfelec, B.; Mallet, B.; Chapus, C.
FEBS Lett. 250, 166-170, 1989
A; Title: Identification of a procarboxypeptidase A-truncated protease E binary complex A; Reference number: S04999; MUID:89325560; PMID:2753124
A; Accession: S04999
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A; Residues: 94-128;123-164 < WEN>
C; Superfamily: trypsin; trypsin homology
C; Superfamily: trypsin; trypsin hydrolase; serine proteinase; zymogen
C; Superfamily: signal sequence #status predicted <SIGN
F;1-17/Domain: activation peptide #status predicted <ACT>
F;29-270/Product: (or 31-270) pancreatic elastase IIIB #status predicted
F;29-230/Domain: trypsin homology <TRY>
F;29-230/Apcaine: trypsin homology <TRY>
F;31-133,121/Active Site: His, Asp, Ser #status predicted
F;114/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;153/Binding site: carbohydrate (Asn) (covalent) #status absent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                 A; Cross-references: GB:M18692; NID:g607029; PIDN:AAA58454.1; PID:g182035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 'G',5-63, 'G',65-78,'W',80-118,'G',120-163,'P',165-270 <SHE>
R:Fletcher, T.S.
Submitted to Genbank, August 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Reference number: A94507
A; Contents: revision to residue 119
A; Accession: A27206
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Matches
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8

Gaps

Indels 12; Length 271;

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Search completed: December 20, 2002, 15:19:50 Job time : 15.6087 secs
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IVNGENAVPGSWPWQVSLQ-DNTG--FHFCGGSLISPNWVVTAAHCQVTPGRHFVVLGEX 57 :1||||:||| |||||| : : |||||||| vvngedavpyswpwqvSlQYekSGSFYHTCGGSLIAPDWVVTAGHCISSSRTYQVVLGEX 88

53

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4

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(without alignments)
864.421 Million cell updates/sec
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1 IVNGENAVPGSWPWQVSLQD......AMYTRVSKFSTWINQVMAYN 231
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                           908470 seqs, 133250620 residues
                                                                                                                                                                                                   US-09-856-319B-4_COPY_34_264

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Maximum DB seq
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/ SIDS2/99datu/geneseq/geneseqp_embl/AA1989 .DAT:
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## STIMMARTES

					CHIMPING	
		æ				
Result		Query				
NO.	Score	Match	Match Length DB ID	DB	υ	Description
			1	1		
-	1252	100.0		2	AAB11711	Mouse serine prote
~	1112	88.8		21	AAB11710	Human serine prote
m	756	60.4		21	AAB54077	Human pancreatic c
4	755.5	60.3		23	AAU82738	Amino acid sequenc
2	750.5	59.9		22	AAB98504	Human chymotrypsin
ø	727.5	58.1	245	21	AAY99596	Bovine chymotrypsi
7	503	40.2		7	AAP61724	Porcine elastase I
æ	503	40.2		æ	AAP70758	Pig pancreas elast
6	500.5	40.0		13	AAR29621	Porcine pancreatic
10	486	38.8		7	AAP60062	Sequence of human

Serine proteases BSSP5, useful in detecting homologs, mutants and

00 0 6 6 6	Human plasminogen. Complete mouse pla Murine plasminogen
44 4	ABB83/95 AAR83959 AAW07585
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## ALIGNMENTS

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BSSP5; serine protease; human; hBSSP5; mouse; mBSSP5; brain; diagnostic marker; antibody; transgenic animal; Alzheimer's disease; epilepsy; cancer: inflammation; infertility; pancreatitis; prostatic hypertrophy.
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                                                                          Mouse serine protease BSSP5 (mBSSP5) SEQ ID NO:4.
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                                                                                                                                                                                                                                                                    Kominami K,
                 AAB11711 standard; Protein; 264
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                                                                                                                                                                                                                            98JP-0347806
                                                                                                                                                                                                                                                (FUSO ) FUSO PHARM IND LTD.
                                                      23-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                    Uemura H, Okui A,
                                                                                                                                                                                                                                                                                      WPI; 2000-400058/34
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                                                                                                                                                                                     02-JUN-2000.
                                     AAB11711;
                                                                                                                                                Mus sp.
RESULT 1
        AAB11711
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Yamaguchi N, Mitsui S;

Kominami K,

Uemura H, Okui A,

(FUSO ) FUSO PHARM IND LTD

99WO-JP06473. 98JP-0347806

19-NOV-1999; 20-NOV-1998;

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The invention relates to novel serine proteases designated BSSP5

(AAB11710-B11711), and to nucleic acids encoding them (AAA61733-A61734).

The invention also relates to vectors and transformants comprising BSSP5 nucleic acids; transgenic animals in which the expression level of BSSP5 nucleic acids; transgenic animals in which the expression level of BSSP5 nucleic and an mBSSP5 knockout mouse. The invention additionally encompasses anti-BSSP5 antibodies and methods of production of such antibodies, methods of BSSP5 detection using the antibodies, and the use of BSSP5 proteins or fragments as diagnostic markers for certain medical conditions or f.g., pancreatitis. A method for detecting pancreatitis comprising measuring BSSP5 concentration in the blood or urine, and a pancreatitis diagnostic agent containing an anti-BSSP5 isolated in a human brain cDNA library using degenerate PCR primers (AAA61745) based on conserved regions of serine proteases. The BSSP5 serine proteases and nuclectides encoding them are useful in detecting homologues, mutants and polymorphic variants in biological samples (e.g., blood, urine, brain, prostate gland, placenta, testis, pancreas and spleen) as diagnostic markers for conditions such as Alzheimer's alsease, epilepsy, cancer, inflammation, infertility, pancreatitis and prostatic hypertrophy. Sequence AAB11711 represents murine BSSP5 human brain and sequence AAB11711 represents
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polymorphic variants as markers for diagnosis of e.g. Alzheimer's disease, epilepsy, cancer and inflammation, using blood, urine, pancreas or other tissues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human serine protease BSSP5 (hBSSP5) SEQ ID NO:2.
                                                                                          Claim 3; Page 55-56; 70pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB11710 standard; Protein; 264 AA
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Matches 231; Conservative
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The invention relates to novel serine proteases designated BSSP5

(AABI1710-B11711), and to nucleic acids encoding them (AAA6733-A61734).

The invention also relates to vectors and transformants comprising BSSP5 nucleic acids; transgenic animals in which the expression level of BSSP5 nucleic acids; transgenic animals in which the expression level of BSSP5 can be varied; and an mBSSP5 knockout mouse. The invention additionally encompasses anti-BSSP5 antibodies and methods of production of such artibodies, methods of BSSP5 detection using the antibodies, and the use of BSSP5 proteins or fragments as diagnostic markers for certain medical conditions, e.g., pancreatitis. A method for detecting mencreatitis comprising measuring BSSP5 concentration in the blood or urine, and a pancreatitis diagnostic agent containing an anti-BSSP5 antibody is also disclosed. Nucleotides encoding BSSP5 were initially isolated in a human brain cDNA library using degenerate PCR primers (AAA61744-A61745) based on conserved regions of serine proteases. The BSSP5 serine proteases and nucleotides encoding them are useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       detecting homologues, mutants and polymorphic variants in biological samples (e.g., blood, urine, brain, prostate gland, placenta, testis, pancreas and spleen) as diagnostic markers for conditions such as Alzheimer's disease, epilepsy, cancer, inflammation, infertility, pancreatitis and prostatic hypertrophy, Sequence AAB11710 represents human BSSP5 (HBSSP5), and sequence AAB11711 represents murine BSSP5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Serine proteases BSSP5, useful in detecting homologs, mutants and oblymorphic variants as markers for diagnosis of e.g. Alzheimer's disease, epilepsy, cancer and inflammation, using blood, urine, pancreas or other tissues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         214 SGGPLVCQKGNTWVLIGIVSWGTKNCNVRAPAVYTRVSKFSTWINQVIAYN 264
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85.7%; Pred. No. 6.3e-90;
ive 22; Mismatches 11
                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 51-52; 70pp; Japanese.
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                                                                                                                                                                    WPI; 2000-400058/34.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       264 AA;
                                                                                                                                                                                           N-PSDB; AAA61733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mBSSP5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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g
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Human; protease; cancer; immune-related disorder; cardiovascular disease; neuronal-associated disease; metabolic disorder; inflammatory disorder; nervous system disorder; sexual dysfunction; pain; mood disorder; hypertension; psychotic disorder; neurological disorder; disorder; viral infection; human immunodeficiency virus; HIV; non-viral infection;

ocular disease; cytostatic; enzyme.

26-JUN-2001; 2001WO-US20171. 26-JUN-2000; 2000US-214047P

WO200200860-A2.

03-JAN-2002.

Homo sapiens.

Amino acid sequence of novel human protease #37.

23-APR-2002 (first entry)

AAU82738;

AAU82738 standard; Protein; 263 AA.

AAU82738

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proteins, called pancreatic cancer antigens, given in AAB54008 to
AAB5466. The human pancreatic cancer antigens have cytostatic,
neuroprotective, nootropic, immunomodulatory, relaxant, contraceptive,
gynaecological, cardiant and antilifammatory activities, and can be used
in gene therapy. The polynucleotide and proteins can be used for
preventing, treating, or ameliorating a medical condition or in assays
for diagnosing a pathological condition or a susceptibility to one in a
subject. Binding partners to the proteins and the activity of the
proteins can be identified. The pancreatic cancer antigens can be used to
detect, treat or prevent pancreatic disorders, especially cancer.
Agonists and antagonists to the antigens can be used to design nucleic
and antagonists to the antigens can be used to design nucleic
and disquistic methods. The proteins can be used to design nucleic
and disquistic methods. The proteins can be used to penerate antibodies
which are used to purify, detect and target the polypeptides, including
both in vivo and in vitro diagnostic and therapeutic methods. The
proteins can be used to treat or prevent neural, immune system, muscular,
reproductive, gastrointestinal, pulmonary, cardiovascular, renal or
proteins can be used to treat or prevent neural, immune system, muscular,
reproductive, gastrointestinal, pulmonary, cardiovascular, renal or
proteins can be used to treat or prevent neural, immune system, muscular,
reproductive, gastrointestinal, pulmonary, cardiovascular, renal or
proteins can be used to the present invention.
                          Humma; pancreas; pancreatic cancer; pancreatic cancer antigen; detection; diagnosis; identification; cytostatic; neuroprotective; nootropic; immunomodulatory; relaxant; contraceptive; gynaecological; antiinflammatory; cardiant; gene therapy; chromosome mapping; linkage analysis; itssue identification; itssue typing; forensic; neural; immune system; muscular; reproductive; gastrointestinal; pulmonary; cardiovascular; renal; proliferative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid that is a pancreatic cancer antigen for preventing, treating, or ameliorating a medical condition, particular pancreatic cancer, or for use in assays for diagnosing a pathological condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAC98773 to AAC99231 encode the human pancreatic cancer associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 11; Page 966; 1379pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                08-MAR-2000; 2000WO-US05989.
                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0124270.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-579444/54.
N-PSDB; AAC98842.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rosen CA, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               192 AA;
                                                                                                                                                                                                                                                                             WO200055320-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                  12-MAR-1999;
                                                                                                                                                                                                                                                                                                                              21-SEP-2000,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to the isolation of novel human proteases, and the nucleic acids encoding them. The sequences of the invention are useful for treating diseases and disorders such ascers (e.g. breast, colon, lung), immune-related diseases and disorders (e.g. inflammatory diseases and asthma), cardiovascular diseases and diseases, metabolic disorders (e.g. dispetes) brain or neuronal-associated diseases, metabolic disorders (e.g. diabetes) central or peripheral nervous system diseases, migraines, pain, sexual dysfunction, mood disorders, attention disorders, cognition disorders, hypotension, psychotic disorders, neurological disorders, hypotension, hypertension, psychotic disorders, neurological disorders, and dyskinesias. (e.g. Alzheimer's disease, parkinson's disease) and dyskinesias. Infections caused by human immunodeficiency virus (HTV), and non-viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 infections such as ocular disease (e.g. glaucoma) and macular degeneration. AAU82702-AAU82760 represent the novel human proteases of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 SNAEPVQVLSIARAITHPNWNANTMNNDLTLLKLASPARYTAQVSPVCLASTNEALPSGL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34 IVNGEDAVPGSWPWQVSLQDKTGFHFCGGSLISEDWVVTAAHCGVRTS-DVVVAGEFDGG 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 IVNGENAVPGSWPWQVSLQDNTGFHFCGGSLISPNWVVTAAHCQVTPGRHFVVLGEYDRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 263;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 1.5e-58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60.3%; Score 755.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 6; Fig 2M; 313pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            263 AA;
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Gaps

60.4%; Score 756; DB 21; Length 192; 84.4%; Pred. No. 9.2e-59; .tve 16; Mismatches 9; Indels (

Conservative

Best Local Similarity Matches 135; Conserv

Query Match

150 TCVTTGWGRLSGVGNVTPAHLQQVALPLVTVNQCRQYWGS 189 TCVTTGWGRISGVGNVTPARLQQVVLPLVTVNQCRQYWGA 160

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g ð

Nucleic acids encoding novel human proteases, useful for useful for treating diseases and disorders such as cancers, immune-related diseases and disorders, cardiovascular disease (e.g. restenosis) and

inflammatory disorders

Caenepeel S;

Sudarsanam S, Manning G,

Whyte D,

Plowman G, Wł Charydczak G;

(SUGE-) SUGEN INC

WPI; 2002-139913/18.

N-PSDB; ABK31780

121 LCATTGWGKTKYNANKTPDKLQQAALPLLSNAECKKSWGRRITDVMICAGASGVSSCMGD 180

SGGPLVCQKGNTWVLIGIVSWGTKNCNIQAPAMYTRVSKFSTWINQVMAYN 231

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TADG-15 is an extracellular serine protease. It was found that TADG-15 is over-expressed in ovarian tumours. TADG-15 protein or its fragments of 9-20 residues that lack TADG-15 protease activity are useful for vaccinating an individual against TADG-15, having, suspected of having or at risk of getting cancer. Furthermore, the TADG-15 gene can be used as a diagnostic or therapeutic target in cancer. The present sequence was used in a sequence homology alignment with the catalytic domain of TADG-15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel extracellular serine protease, termed tumor antigen-derived gene 15 protein overexpressed in carcinomas and DNA encoding it, for diagnosis, treatment, prevention of cancer, particularly breast,
                                             121 TCVTTGWGRISGVGNVTPARLQQVVLPLVTVNQCRQYWGARITDAMICAGGSGASSCQGD 180
93 SDEENIQVLKIAKVFKNPKFSILTVNNDITLLKLATPARFSQTVSAVCLPSADDDFPAGT 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 231;
                                                                                                                                                                                                                                                                                                                             Human; TADG-15; cytostatic; vaccine; ovarian tumour; cancer;
tumour antigen-derived gene 15; serine protease; chymotrypsin.
                                                                                                          SGGPLVCQKGNTWVLIGIVSWGTKNCNIQAPAMYTRVSKFSTWINQVMAYN 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61; Indels
                                                                                                                                                                                                                                                                                                 Human chymotrypsin serine protease catalytic domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 750.5; DB 2;
Pred. No. 3.5e-58;
5; Mismatches 61,
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                                                                                                                                                                                                      AAB98504 standard; Protein; 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59.9%;
58.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-OCT-2000; 2000WO-US29095.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0421213.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tanimoto H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYAR-) UNIV ARKANSAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-381031/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       231 AA;
                                                                                                                                                                                                                                                                                                                                                                                                            WO200129056-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ovarian cancer
                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-0CT-1999;
                                                                                                                                                                                                                                                                  03-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    O'Brien TJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                         26-APR-2001
                                                                                                                                                                                                                                   AAB98504;
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                                                                                                                                                                        RESULT 5
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a review of sequence homologies of several plasminogen activators.

Plasminogen is the principal serine protease zymogen in the extracellular fluids of vertebrates. Its active form, plasmin, is implicated in pericellular proteolysis associated with a wide range of physiological and pathological processes. Plasminogen expression is cyclusted by plasminogen activators which hydrolyse a peptide bond in plasminogen to convert it to plasmin or form tight binding complexes with plasminogen to convert it to plasmin or form tight binding complexes with plasminogen to spontaneously convert it to plasmin. The sequence homology analysis has identified a six amino acid peptide involved in plasminogen activation. This peptide is particularly useful when inserted between amino acid residues 644 and 645 of full length human confirmation. Those periods activators have been made based upon the plasminogen activation. Freegonition site of plasminogen binding proteins. The polypeptides are useful in preparing thrombolytic agents for treating blood clotting disorders such as heart attack.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Polypeptide with plasminogen activator activity useful as thrombolytic agent for treating blood clot disorders e.g. heart attack, comprises 10 amino acid peptide fragment for recognition or activation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SNAEPVQVLSIARAITHPNWNANTMNNDLTLLKLASPARYTAQVSPVCLASTNEALPSGL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |::| :| || || :: :|: || :| || || || || :: :| SSSERIQKLKIAKVFKNSKINSLTINNDITLLKLSTAASFSGIVSAVCLPSASDDFAAGT 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 IVNGENAVPGSWPWQVSLQDNTGFHFCGGSLISPNWVVTAAHCQVTPGRHFVVLGEYDRS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16 IVNGEEAVPGSWPWQVSLQDKTGFHFCGGSLINENWVVTAAHCGVTTS-DVVVAGEFDQG 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is bovine chymotrypsinogen. It was included in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1;
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Indels
                                                                                                                                                                                                                                                         thrombolytic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67;
                                                                                                                                                                                                                                                       Bovine; plasminogen activator; cardiant; thro
heart attack; stroke; blood clotting disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 727.5; DB
Pred. No. 4e-56;
2; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 35-36; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (OKLA-) OKLAHOMA MEDICAL RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32;
                                                                                                       AAY99596 standard; protein; 245
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56.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tang JJN;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          98US-0110588
                                                                                                                                                                              13-SEP-2000 (first entry)
                                                                                                                                                                                                                    Bovine chymotrypsinogen A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 56.7%
Matches 131; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-422975/36.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zhang XC,
                                                                                                                                                                                                                                                                                                                                               WO200032759-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                        06-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    plasminogen
                                                                                                                                                                                                                                                                                                              Bos taurus.
                                                                                                                                          AAY99596;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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             181
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                                                                                    AAY99596
ID AAY9
                                                                     RESULT 6
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121 TCVTTGWGRISGVGNVTPARLQQVVLPLVTVNQCRQYWGARITDAMICAGGSGASSCQGD 180

SNAEPVQVLSIARAITHPNWNANTMNNDLTLLKLASPARYTAQVSPVCLASTNEALPSGL 120

1 IVNGENAVPGSWPWQVSLQDNTGFHFCGGSLISPNWVVTAAHCQVTPGRHFVVLGEYDRS 60 

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Pancreas elastase prodn. used to improve lipoprotein metabolism comprises isolating RNA coding elastase, synthesising single and double chain cDNA and introducing recombinant into host
                                                                                                                                                                                                     /note= "May be absent"
                                                                                                                                                                       Location/Qualifiers 2..16
                          AAP70758 standard; Protein; 269
                                                                                                                             Lipoprotein metabolism; lipid
                                                                                                                                                                                                                                                                                                          85JP-0138494.
                                                                                                                                                                                                                                                                                 85JP-0138494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 107; Conservative
                                                                                                     Pig pancreas elastase-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                           WPI; 1987-040875/06.
                                                                                                                                                                                                                                                                                                                                   (SANY ) SANKYO KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      269 AA;
                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAN71121
                                                                                                                                                                                          Misc-difference
                                                                           19-APR-1991
                                                                                                                                                                                                                                JP62000276-A
                                                                                                                                                                                                                                                                                 25-JUN-1985;
                                                                                                                                                                                                                                                                                                          25-JUN-1985;
                                                                                                                                                                                                                                                        06-JAN-1987.
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                                                   AAP70758;
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 RESULT 8
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د
 TCVTTGWGRISGVGNVTPARLQQVVLPLVTVNQCRQYWGARITDAMICAGGSGASSCQGD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DRSSNAEPVQVLSIARAITHPNWNANTMN-`-NDLTLLKLASPARYTAQVSPVCLASTNEA 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LPSGLTCVTTGWGRISGVGNVTPARLQQVVLPLVTVNQCRQ--YWGARITDAMICAGGSG 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -ASSCQGDSGGPLVCQKGN-TWVLIGIVSWGTK-NCN-IQAPAMYTRVSKFSTWINQVMA 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               208 IISSCNGDSGGPLNCQGANGQWQVHGIVSFGSSLGCNYYHKPSVFTRVSNYIDWINSVIA 267
                 The porcine elastase product may be efficiently expressed from a transformed host such as colibacillus or yeast, yielding the product more efficiently than spleen extraction.

See also J61192288.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 IVNGENAVPGSWPWQVSLQ-DNTG--FHFCGGSLISPNWVVTAAHCQVTPGRHFVVLGEY 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12;
                                                              SGGPLVCQKGNTWVLIGIVSWGTKNCNIQAPAMYTRVSKFSTWINQVMAYN 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40.2%; Score 503; DB 7; Length 269; 44.2%; Pred. No. 2.5e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biological prepn. of pig elastase II - using DNA with sequence coding for specified aminoacid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41; Mismatches
                                                                                                                                          Ź
                                                                                                                                       AAP61724 standard; Protein; 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Fig 1; 11pp; Japanese.
                                                                                                                                                                                                                                                                                                                                             85JP-0034050
                                                                                                                                                                                                                                                                                                                                                                     85JP-0034050
                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 44.2
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                              (KIRI ) KIRIN BREWERY KK.
                                                                                                                                                                                                                                        Colibacillus; yeast.
                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1986-262895/40.
N-PSDB; AAN60919.
                                                                                                                                                                                                                 Porcine elastase II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      269 AA;
                                                                                                                                                                                                                                                                                          JP61192289-A.
                                                                                                                                                                                                                                                                                                                                             22-FEB-1985;
                                                                                                                                                                                                                                                                                                                                                                     22-FEB-1985;
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                                                                                                                                                                                                                                                                                                                    26-AUG-1986.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NN 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YN 231
                                                                                                                                                                                                                                                                    Sus scrofa.
                                                                                                                                                               AAP61724;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                       135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             268
121
                                                181
                                                                       195
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116 LPSGLTCVTTGWGRISGVGNVTPARLQQVVLPLVTVNQCRQ--YWGARITDAMICAGGSG 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      174 -ASSCQGDSGGPLVCQKGN-TWVLIGIVSWGTK-NCN-IQAPAMYTRVSKFSTWINQVMA 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    208 IISSCNGDSGGPLNCQGANGQWQVHGIVSFGSSLGCNYYHKPSVFTRVSNYIDWINSVIA 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58 DRSSNAEPVQVLSIARAITHPNWNANTMN--NDLTLLKLASPARYTAQVSPVCLASTNEA 115
                                                                                                                                                                                                                                                                                                                                                                          1 IVNGENAVPGSWPWQVSLQ-DNTG--FHFCGGSLISPNWVVTAAHCQVTPGRHFVVLGEY 57
                                                   Sequence encoding pancreas elastase may be used to transform an expression system. The product is useful in rejuvenating the elasticity of the arterial wall, and improving unusual serum lipid levels and lipoprotein metabolism.
                                                                                                                                                                                                                                                                                                                                                                                                                  29 VVGGEDARPNSWPWQVSLQYDSSGQWRHTCGGTLVDQSWVLTAAHCISSSRTYRVVLGRH
                                                                                                                                                                                                                                                                                                                      12;
                                                                                                                                                                                                                                                            Length 269;
                                                                                                                                                                                                                                                                                                                      82; Indels
                                                                                                                                                                                                                                                            40.2%; Score 503; DB 8; 44.2%; Pred. No. 2.5e-36;
                                                                                                                                                                                                                                                                                                                      41; Mismatches
Disclosure; Page 480; 18pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR29621 standard; Protein; 253 AA.
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AAR29621
ID AAR2
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269 AA;
                                                                                                                                           (SANY ) SANKYO KK.
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         Homo sapiens
                                                                                                   27-APR-1985;
26-JUL-1985;
02-DEC-1985;
                                                                07-APR-1986;
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                                                                                   23-OCT-1985
                                                                                            05-APR-1985
                                             22-OCT-1986
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                          EP198645-A.
                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               172 SGASSCQGDSGGPLVCQKGN-TWVLIGIVSW-GTKNCN-IQAPAMYTRVSKFSTWINQVM 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DRSSNAEPVQVLSI--ARAITHPNWNANTMN--NDLTLLKLASPARYTAQVSPVCLASTN 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                 72 DRSENEGFEQVIPINAGDLFVHPRWNSNCVSCGNDIALVKLSRSAQLGDKVQLACLPPAG 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    114 EALPSGLTCVTTGWGRISGVGNVTPARLQQVVLPLVTVNQCRQ--YWGARITDAMICAGG 171
                                                                                                                                                                                                                                                                                                                                                                                                     12 VVNGEDAVPYSWPWQVSLQYEKNGVFQHTCGGSLIAPDWVLTAGHCISSSLTYQVVLGEY 71
                                                                                                                                                                                                                                                                                                                                                                                          1 IVNGENAVPGSWPWQVSLQ-DNTGF--HFCGGSLISPNWVYTAAHCQVTPGRHFVVLGEY 57
                                                                Pig; swine; bile acid; gall bladder; bile acid secretion promoters;
                                                                                                                                                                                                                                                                                   This sequence represents porcine pancreatic elastase III. It was expressed in E. coli YA21 using the expression vector pELE001. It may be used in bile acid secretion promoters and liver function
                                                                                                                                                                                                                                                                                                                                                     40.0%; Score 500.5; DB 13; Length 253; 43.2%; Pred. No. 3.9e-36; Live 42; Mismatches 82; Indels 13;
                                                                                                                                                                                                                                      Pig pancreas elastase protein - used in bile acid secretion promoters and liver function improvers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence of human pancreatic elastase IIA encoded on pH2E2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAP60062 standard; Protein; 269 AA.
                                                                                                                                                                                                                                                                  Claim 1; Page 8; 10pp; Japanese.
                                             Porcine pancreatic elastase III.
                                                                          liver function improvers; ss
                                                                                                                                                                       91JP-0092069
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                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                         (SANY ) SANKYO CO LTD.
                                                                                            Sus scrofa domestica.
                                                                                                                                                                                                           WPI; 1992-428826/52.
                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                    253 AA;
                                                                                                                                                                                                                      N-PSDB; AAQ31724
                                                                                                              JP04325090-A.
                                                                                                                                                    23-APR-1991;
                                                                                                                                                                       33-APR-1991;
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                          30-APR-1993
                                                                                                                                 13-NOV-1992
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Matches 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              229 A 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                251 A 251
                                                                                                                                                                                                                                                                                                                                     Seguence
        AAR29621;
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ID AAP
XX AC AAP
XX O6-
XX O6-
XX SEQ
XX EDZ
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58 DRSSNAEPVQVLSIARAITHPNWNANTMN-·NDLTLLKLASPARYTAQVSPVCLASTNEA 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29 VVGGEEARPNSWPWQVSLQYSSNGKWYHTCGGSLIANSWVLTAAHCISSSRTYRVGLGRH 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 IVNGENAVPGSWPWQVSLQDNTG---FHFCGGSLISPNWVVTAAHCQVTPGRHFVVLGEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           116 LPSGLTCVTTGWGRISGVGNVTPARLQQVVLPLVTVNQCRQ--YWGARITDAMICAGGSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The genetically engineered prod. can eliminate the dependency on human pancreas supplies for the elastase, and avoids antibody formation and possibility of anaphylaxis using porcine elastase.
                                                                                                                                                                                                                                                                                                                                                                                                                   New genetically engineered human pancreatic elastase - obtd.
using hosts modified DNA coding for enzyme
                                                                                                                                                                                                                                                              Ohmine T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 7; Length 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 38.8%; Score 486; DB 7; Length 26 Best Local Similarity 43.0%; Pred. No. 8e-35; Matches 104; Conservative 41; Mismatches 85; Indels
                                                                                                                                                                                                                                                                'n
                                                                                                                                                                                                                                                                Eurukawa
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                                                                                                                                                                                                                                                              Kawashima I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example; Page 14-15; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAP60061 standard; Protein; 242 AA.
                                             85JP-0236686.
85JP-0072308.
85JP-0091986.
85JP-0163964.
85JP-0271128.
86EP-0302557
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                                                                                                                                                                                                                                                           Takiguchi Y, Tani T,
Ohsumi J;
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N-PSDB; AAN60076.
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30-MAR-2001; 2001WO-US08631
                                                                       SANY ) SANKYO
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                                                                                     rakiguchi Y,
                                       27-APR-1985;
26-JUL-1985;
02-DEC-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
        07-APR-1986;
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                        23-OCT-1985
05-APR-1985
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                                                                                                                                                                                                                                                                                                                                                                                                   NN 252
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                                                                                              Ohsumi J;
                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                    251
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                                                                                                                                                                                                                                                                                                                                                                           SGASSCOGDSGGPLVC-OKGNTWVLIGIVSW-GTKNCNI-QAPAMYTRVSKFSTWINQVM 228
                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                        : ||: | |||||: | : ||:||: ||:|| |
DILPNETPCYITGWGRLYTNGPL-PDKLQEALLPVVDYEHCSRWNWWGSSVKTMVCAGG
                                                                                                                                                                                                                                                                                                                                            EALPSGLTCVTTGWGRISGVGNVTPARLQQVVLPLVTVNQCRQ--YWGARITDAMICAGG
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                                                                                                                                                                                                                                                                13;
                                                                                                                                                                                                                                               DB 7; Length 242;

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                                                                                                             Ohmine T;
                                                                                                                                                                                                                                                                 86; Indels
                                                                                                                                                          New genetically engineered human pancreatic elastase using hosts modified DNA coding for enzyme
                                                                                                            Eurukawa H,
                                                                                                                                                                                                                                               38.5%; Score 481.5; DB 7 42.7%; Pred. No. 1.7e-34; tive 39; Mismatches 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence of human pancreatic elastase IIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Enzyme; serum lipoprotein metabolism
                                                                                                            Kawashima I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAP60058 standard; Protein; 252 AA
                                                                                                                                                                                 Claim 2; Page 8; 45pp; English
                                            85JP-0236686.
85JP-0072308.
85JP-0091986.
85JP-0163964.
85JP-0271128.
                               86EP-0302557
                                                                                                                                                                                                                                                        Best Local Similarion
Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                            rakiguchi Y, Tani T;
                                                                                                                                  WPI; 1986-280300/43.
                                                                                                                                                                                                                                 242 AA;
                                                                                            (SANY ) SANKYO KK.
                                                                                                                                           N-PSDB; AAN60075
                                                             27-APR-1985;
26-JUL-1985;
02-DEC-1985;
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                              07-APR-1986;
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               22-OCT-1986
EP198645-A
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                                                                                                                                                                                                                                  Sequence
                                                                                                                     Ohsum1 J;
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DRSSNAEPVQVLSIARAITHPNWNANTMN--NDLTLLKLASPARYTAQVSPVCLASTNEA 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LPSGLTCVTTGWGRISGVGNVTPARLQQVVLPLVTVNQCRQ--YWGARITDAMICAGGSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             174 A-SSCQGDSGGPLVCQKGN-TWVLIGIVSWGTK-NCN-IQAPAMYTRVSKFSTWINQVMA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human pancreas supplies for the elastase, and avoids antibody formation and possibility of anaphylaxis using porcine elastase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37.7%; Score 471.5; DB 7; Length 252; 42.6%; Pred. No. 1.4e-33; tive 41; Mismatches 85; Indels 13
                                                                                                                                                                                                                                                                                                                                                                                                genetically engineered human pancreatic elastase - obtd.
ng hosts modified DNA coding for enzyme
                                                                                                                                                                                                                                                 Ohmine
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                                                                                                                                                                                                                                                 Kawashima I,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 2; Page 3-4; 45pp; English.
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                                            85JP-0236686.
85JP-0072308.
85JP-0091986.
85JP-0163964.
85JP-0271128.
86EP-0302557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 42.69
Matches 103; Conservative
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                                                                                                                                                                                                                                                                                                                  WPI; 1986-280300/43.
N-PSDB; AAN60072.
                                                                                                                                                                                                                                                 Tani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              252 AA;
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Plasminogen; human; Kringle 5 peptide; anti-angiogenesis agent; cancer metastatic solid tumour; carcinoma; sarcoma; lymphoma; haemangioma; psoriasis; arthritis; macular degeneration; diabetic retinopathy; autoimmune disease; ocular disease; capillary proliferation; therapy; kringle 5 receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58 DRSSNAEPVQVLSIARAITHPNWNANTMN--NDLTLLKLASPARYTAQVSPVCLASTNEA 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 174 A-SSCQGDSGGPLVCQKGNTWVLI-GIVSWGTK-NCN-IQAPAMYTRVSKFSTWINQVWA 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 IVNGENAVPGSWPWQVSLQDNTG---FHFCGGSLISPNWVVTAAHCQVTPGRHFVVLGEY 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  149 LPNNYPCYVTGWGRLQTNGAV-PDVLQQGRLLVVDYATCSSSAWWGSSVKTSMICAGGDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 116 LPSGLTCVTTGWGRISGVGNVTPARLQQVVLPLVTVNQCRQ--YWGARITDAMICAGGSG
                                                                                                                                                                                                                                                                                                                                                         Biologically producing human elastase ii - using DNA chain with biological prodn. capability for human elastase II.
                                                                                                                                                                                                                                                                                                                                                                                                                                           The human elastase product may be efficiently expressed from transformed host such as colibacillus or yeast, yielding the more efficiently than spleen extraction.

See also J61192289.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37.5%; Score 469; DB 7;
42.6%; Pred. No. 2.5e-33;
live 40; Mismatches 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW34285 standard; protein; 791 AA.
                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Fig 1-2; 19pp; Japanese.
                                                                                                                                                                                                     85JP-0034049
                                                                                                                                                                                                                                       85JP-0034049
23-OCT-1991 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                        WPI; 1986-262894/40.
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Matches 103; Conserv
                                 Human elastase II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               269 AA;
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                                                                                                                                                                                                                                                                                                                        N-PSDB; AAN60706
                                                                 Colibacillus;
                                                                                                    Homo sapiens.
                                                                                                                                  JP61192288-A.
                                                                                                                                                                                                                                       22-FEB-1985;
                                                                                                                                                                                                     22-FEB-1985;
                                                                                                                                                                    26-AUG-1986
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97 NLYVAE-----SGSLAMSSVSKIVVHKDWNFNQISKGNDIALLKLANPVSLTDKIQLAC 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  151 FPPAGTILPNNYPCXVTGLGESCRTNGAVPDVLQQGRLLAVDYATCSSSAWWGSSVKTSM 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       211 ICAGGDGVISSCNGDSGGPLNCQASDALWQVHGIVSFGSRLGCNYYHKPSVFTRVSNYID 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51 FVVLGEYDRSSNAEPVQVLSIARAITHPNWNANTMN--NDLTLLKLASPARYTAQVSPVC 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  109 LASTNEALPSGLTCVTTGWGRISGVGNVTPARLQQVVLPLVTVNQCRQ--YWGARITDAM 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   167 ICAGGSGA-SSCOGDSGGPLVCQKGNT-WVLIGIVSWGTK-NCN-IQAPAMYTRVSKFST 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 IVNGENAVPGSWPWQVSLQDNTG---FHFCGGSLISPNWVVTAAHC-----QVTPGRH 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37.6%; Score 471; DB 22; Length 279; 41.0%; Pred. No. 1.7e-33; tive 39; Mismatches 84; Indels 2.
                                                                                                                                                                                                                                                                                                      The invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                     Claim 20; SEQ ID No 50872; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAP61723 standard; Protein; 269 AA.
                                                                                                  Tang YT;
              31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                 Drmanac RT, Liu C,
                                                                                                                                  WPI; 2001-639362/73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                279 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       223 WINQVMAYN 231
                                                                 (HYSE-) HYSEQ INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             specification
                                                                                                                                                                                                                                       biodiversity
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Sequence Query Match

Local Matches

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AAP61723;

AX XX

RESULT 14 AAP61723

8

12; Gaps

87;

Length 269; Indels

a product

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This sequence represents human plasminogen. Fragments of this sequence can be used in the compounds of the invention. Kringle 5 (K5) peptide fragments homologous to this sequence, are anti-anglogenesis agents. Specifically for treating or preventing cancer, particularly primary or metastatic solid tumours, carcinomas, sarcomas, lymphomas, haemangiomas. They can also be used for treating or preventing psoriasis, arthritis. They can also be used for treating or preventing psoriasis, arthritis. They can also be used to treat autoimmune or coular diseases, capillary proliferation within atherosclerotic plaque, haemophiliac joints, wound granulation, ulcers etc., also as contraceptives that inhibit ovulation and establishment of the placenta. K5 antisear or (art)agonists can be used similarly, optionally coupled to cytotoxic agents. Antagonists may be used to induce andiogenesis, e.g. for wound healing. The K5 peptides are also used to raise specific antibodies (Ab), for diagnosis and for afinity purification of K5 receptors. The K5 receptors may then be captually the peptides in biological samples. The K5 peptides (and K5 fission proceins) selectively inhibit proliferation of endothelial cells with low toxicity against normal cells. Typically they have then kingle 1-4 peptides.
                                                                                                                                                                                                                                                                                                                                           New kringle 5 peptide(s) and fusion proteins derived from plasminogen - useful as anti-angiogenesis agents for treating cancer, psorlasis, arthritis etc., including gene therapy
                                                                                                                                                                                                                                                                   Davidson DJ, Gubbins EJ, Wang J;
                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 11; Fig 1; 78pp; English.
                                                                                                                               97WO-US07700
                                                                                                                                                                   97US-0832087.
                                                                                                                                                                                                                                                                                                     WPI; 1997-558670/51.
                                                                                                                                                                                                                             (ABBO ) ABBOTT LAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            791 AA;
               Homo sapiens
                                                   WO9741824-A2
                                                                                                                               05-MAY-1997;
                                                                                                                                                                   03-APR-1997;
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                                                                                         13-NOV-1997
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′, 58 DRSSNAEP-VQVLSIARAITHPNWNANTMNNDLTLLKLASPARYTAQVSPVCLASTNEAL 116 117 PSGLTCVTTGWGRISGVGNVTPARLQQVVLPLVTVNQCRQY--WGARITDAMICAG--GS 172 Ouery Match 37.2%; Score 465.5; DB 18; Length 791; Best Local Similarity 41.8%; Pred. No. 1.8e-32; Matches 100; Conservative 30; Mismatches 92; Indels 17; Gaps 1 IVNGENAVPGSWPWQVSLQDNTGFHFCGGSLISPNWVVTAAHC---QVTPGRHFVVLGEY 57 173 GASSCOGDSGGPLVCQKGNTWVLIGIVSWGTKNCNIQAPAMYTRVSKFSTWINQVMAYN 231 733 g õ 윱 ò g ò ö

Search completed: December 20, 2002, 15:16:43 Job time : 36.6087 secs

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December 20, 2002, 15:14:08; Search time 4.08696 Seconds (without alignments) 1663.721 Million cell updates/sec
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GenCore version 5.1.3
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166
1 MLLLSLTLSLVLLGSSWGCGVPAITPALSYNQR 33
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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					SUMMARIES	
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14	55.5	33.4		S	Q9V3B9	Q9v3b9 drosophila
15	55.5	33.4		17	097255	Q97z55 sulfolobus
. 16	55	33.1		16	O8ZLR7	O8zlr7 salmonella

082390 salmonella 094aj4 arabidopsis 095xe9 arabidopsis 095xe9 arabidopsis 09fw90 oryza sativ 08xt78 raistonia s 09fea3 oryza sativ 08xb72 yersinia pe 043752 citrus sine 043752 citrus sine 0491053 simian herp 091053 simian herp 091053 simian herp 091053 samian herp 091054 samian herp 09256 cavia porce 08xx88 oryza sativ 080739 arabidopsis 055767 chilo iride 090031 equus cabal 095188 streptomyce 096736 drosophila 094744 homo sapien 094316 rattus ratt	ALIGNMENTS	264 AA. juence update) notation update)	Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus.	P SECUENCE FROM N.A.  STRAIN-C57BL/61; TISSUE-PANCREAS;  MEDLINE-21085660; PubMed-11217851;  A Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishli Y.,  A Arakawa T., Fara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  A Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,  A Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,  A Azawa K., Matsuda H.A., Ashburner M., Baralov S., Casawant T.,  A Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  Schriml L.M., Staubli F., Suzuki R., Tomita M., Magner L., Mashio T.,  Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  A Sacaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.F.,  A Suzuki H., Toyo-oka K., Wang K.H., Weltz C., Whittaker C., Willming L.,  Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,  Hayashizaki Y.;  Refunctional annotation of a full-length mouse cDNA collection.";  "Functional annotation of a full-length mouse cDNA collection.";  "Ruther 409:685-690(2001).  -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE  TRYPSIN FAMILY.
0823G0 094AJ4 095AJ4 095AJ7 095K99 095K178 095BJ3 082BJ2 091039 081039 081039 081039 081039 081039 081039 081039 081039 081039 081039 081718 081718 081718	ALIG	PR] Treat Jast	a; Crania a; Sciuro	CREAS; 21781; bata K., K. Shi Y., K. Shi Y., K. Sori T., Ba hburner M hhurner M T., Mikalı UZUKİ R., M., ADDO JOBA N., G Jetcher C Shamann M., Id M., Too, Id M.,
110 100 100 100 100 100 100 100 100 100		17, 17, 21,	Chordata; Rodentia;	PPANC Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt Shilt
24 26 26 27 27 27 27 27 27 27 27 27 27 27 27 27		RELIMINARY. TrEMBLrel. TrEMBLrel. Protein. POOtein. (Mouse).	a; Chora; Rode	TISSUE- Pubmec Wa A., Rid A., Rid A., Rid A., Ge an H.A., Ge an H.A., Matri General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F General F
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sp_fung1:*
sp_human:*
sp_invertebrate:*
sp_mamma1:*

SPTREMBL_21:*

Database :

sp_organelle:* sp_phage:*

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UNKNOWN_1
PROSITE; PS00134; TRYPSIN_HIS; PROSITE; PS00135; TRYPSIN_SER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRYPSIN FAMILY.
EMBL; AB020757; BAB20287.1;
HSSP; P00766; 4CHA.
                                          Hydrolase; Serine protease.
SEQUENCE 264 AA; 28167 M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hydrolase; Serine protease.
                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 33; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEROPS; S01.256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTRL OR CTRA1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chymopasin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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Q9ER05
                                                                                                                                                                                                                                                                                                      RESULT 3
    S W DR
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KRAIN-C57BL/64; TISSUB-TONGUE;

KRANI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Ruchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Browstein M.J., Bult C., Fletcher C., Fuljita M., Gariboldi M.,

Brons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Nyanshaw-Booris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Nachinalia V., Vandy K., Kawaji H., Kohtsuki S.,

Nachinalia V., Kawai V., Kawai V., Kawaji H., Kohtsuki S.,

Nachinalia V., Kawai V., Kawaji H., Kohtsuki S.,

Nachinalia V., Kawai V., Kawaji H., Kohtsuki S.,

Nachinalia V., Vandy K., Kawaji H., Kawai V., Kawai
                                                                                                                                                                                                                                                                                                                                                                    Gaps
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-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                        Length 264;
                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                28151 MW; 1D979719E07C16DE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                        100.0%; Score 166; DB 11;
100.0%; Pred. No. 2.1e-14;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                          1 MLLLSLTLSLVLLGSSWGCGVPAITPALSYNOR 33
                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MLLLSLTLSLVLLGSSWGCGVPAITPALSYNQR 33
                                                                                                                                              PRINTS; PRO0722; CHYMOTRYPSIN.
SMART; SMO0202; TRYP_SRS; 1.
PROSITE; PS00134; TRYPSIN_DOW; 1.
PROSITE; PS00135; TRYPSIN_HIS; UNKNOWN_1.
Hydrolase; Serine procease.
SEQUENCE 264 AA; 28151 WW; 1D979719E0
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MGD; MGI:88558; Ctrl.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
                                   MEDOFS; SOL.256; --.
MGD; MGI:88558; Ctrl.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
Pfam: PF00089; trypsin; l.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
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PROSITE; PS50240; TRYPSIN_DOM; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AK009019; BAB26029.1;
BAB24967.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-UN-2001 (TrEMBLrel, 17
01-UN-2001 (TrEMBLrel, 15
01-UN-2002 (TrEMBLrel, 21
1810004D15R1k protein.
CTRL OR 1810004D15R1K.
                                                                                                                                                                                                                                                                                                                                                                  33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
AK007333; BAB
P00766; 4CHA.
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                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
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                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                    Matches
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Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
Mammalia; Eutheria; Rodentia; Sciurognath1; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
TISSUE=RAT PANCREAS;
Sogame Y., Mitsui S., Kataoka K., Kashima K., Kato M., Sakagami J.,
Yamaguchi N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Molécular cioning of rat chymopasin.";
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
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                                                         Length 264;
                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
28167 MW; 1D979469A07056C2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28116 MW; F9ED5D210FD3500E CRC64;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Chymopasin (Chymotrypsin A CTRA-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                     01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 166; DB 11; 100.0%; Pred. No. 2.1e-14;
                                                      Score 166; DB 11;
Pred. No. 2.1e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        264 AA.
                                                                                                                                                                                                                                                                                                                                                                                  264 AA
                                                   Ouery Match
100.0%; Score 166; D
Best Local Similarity 100.0%; Pred. No. 2.1
Matches 33; Conservative 0; Mismatches
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33; Conservative 0; Mismatches
                                                                                                                                                                         1 MLLLSLTLSLVLLGSSWGCGVPAITPALSYNQR 33
                                                                                                                                                                                                        1 MILLSLTLSLVLLGSSWGCGVPAITPALSYNQR 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00722; CHYMOTRIPSIN.
SMART; SM0020; Tryp_SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
PROSITE; PS00135; TRYPSIN_ESR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00089; trypsin; 1.
                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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Conservative
                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   2200008D09Rik protein.
2200008D09RIK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
                                                                                                                                                                                                                               Best Local Similarity
Matches 14; Conserv
 TRYPSIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S01.152;
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01-JUN-2001 (
01-JUN-2002 (
                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                09D8X8;
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                                                                                                                                                                                                                                                                                                                                        RESULT 6
Q9D8X8
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Arawar T., Hara A., Shibata K., Yoshino M., Ttoh M., Ishli Y.,
Arawar T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
A Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Rieschmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
Ruehl P., Lewis S., Matsuo Y., Nikaido I., Resole G., Quackenbush J.,
A Schriml L.M., Staubli F., Suzuki R., Tomita M., Ragner L., Washio T.,
Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Askainoich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
Nordone P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Androne P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Whynibay-Boolis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                 Bjoernslett M.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
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                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 166; DB 11; Length 264; 100.0%; Pred. No. 2.1e-14;
                                                                                                                                                                                                                                                                                                                                                                                Indels
            "Molecular cloning of mouse chymopasin.";
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                          28135 MW; 1D979709A07056C2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      263 AA
                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                        1 MLLLSLTLSLVLLGSSWGCGVPAITPALSYNQR 33
                                                                                                                                                                                                                                                                                                                                                                                                        1 MLLLSLTLSLVLLGSSWGCGVPAITPALSYNQR 33
                                                                                                                                                                                                                           Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPS; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
PROSITE; PS00135; TRYPSIN_HIS; UNKNOWN_1.
PROSITE; PS00135; TRYPSIN_SER; 1.
                                                                                                                                                                                 MGD: MGI.88558; Ctrl.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                 STRAIN-129S6/SVEVTAC; TISSUE-SPLEEN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=C57BL/6J; TISSUE=SPLEEN;
MEDLINE=21085660; Pubmed=11217851;
                                                                                                                               EMBL; AB016228; BAB20275.1; -. EMBL; AF236365; AAL11034.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -JUN-2001 (TrEMBLrel. 17, -JUN-2001 (TrEMBLrel. 17, -JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                               33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
Mitsui S., Yamaguchi N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2200008D09R1k protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
                                                                                                                                                            P00766; 4CHA.
                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                           264 AA;
                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                         MEROPS; S01.256;
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                                                                              Bloernslett M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2001
                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                      Query Match
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Q9DC86
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Gaps
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Nature 409:685-690(2001).
--- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
TRYPSIN FAMILY
BRAILS: BAB25112.1;
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HSSP: P00766; 1GCT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                      42.8%; Score 71; DB 11; Length 263; 48.3%; Pred. No. 0.11;
                                                                                                                                                                                                                                          Hydrolase; Serine protease.
SEQUENCE 263 AA; 27821 MW; 2620A27AFBA5D04D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel. 17, Created)
(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                             10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  263 AA.
                                     MEROPS, SOI.152;
MGD; MGI:1913723; 2200008D09R1K.
INTERPRO; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00089; trypsin, 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMARR; SMO07020; TRYP_SPC. 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS50134; TRYPSIN_HIS; UNKNOWN_I.
PROSITE; PS00135; TRYPSIN_SER; 1.
                                                                                                                                                                                                                                                                                                                                             5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGD; MGI:1913723; 2200008D09Rik.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
                                                                                                                                                                                                                                                                                                                                                                                     1 MLLLSLTLSLVLLGSSWGCGVPAITPALS 29
                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-PANCREAS;
MEDLINE-21085660; PubMed-11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPc; 1.
EMBL; AK003060; BAB22539.1; -. HSSP; P00766; 1GCT.
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Query Match
Best Local Similarity 48.3%;
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P00763; 1DPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=2214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEROPS; S01.256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=PANCREAS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=8255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q8THZO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q8THZ0
                                                                                                                                                                                                                                                                                       09W7Q4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MA4368
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                                                                                                                                                                                                                                           RESULT 8
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                                                                                                                                                                                                                                                              Q9W7Q4
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                                                                                                                                                                                               ö
                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 400:685-690(2001).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                               ö
                                                                                                                                              Score 71; DB 11; Length 263; Pred. No. 0.11;
                                                                                                                                                                                          10; Indels
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
PROSITE; PS00135; TRYPSIN_SER; 1.
Hydrolase; Serine prortease; Serine professe; Serine Secouror 263 AA; 27898 WW; C0638FB8F905A92F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28C4487AF1A26B27 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-C57BL/6J; TISSUE-STOMACH, SPLEEN, AND PANCREAS; MEDLINE-21085660; PubMed-11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                             263 AA.
                                                                                                                                                                                            5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00089; trypsin; 1.
SMARN'S PR00722; CHYMOTRYPEIN.
SMARP: SM00020; Tryp_SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
PROSITE; PS00135; TRYPSIN_SER; 1.
Hydrolase; Serine protease.
                                                                                                                                                                                                                                           1 MLLLSLTLSLVLLGSSWGCGVPAITPALS 29
                                                                                                                                                                                                                                                                   InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
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EMBL, AK001079; BAB22553.1; --
EMBL, AK007765; BAB25241.1; --
EMBL, AK00815; BAB25280.1; --
EMBL, AK008729; BAB25861.1; --
EMBL, AK00888; BAB25861.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGD; MGI:1913723; 2200008D09Rik
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2002 (TrEMBLrel. 17, 01-JUN-2002 (TrEMBLrel. 21, 2200008D09R1k protein.
                                                                                                                                              Query Match 42.8%;
Best Local Similarity 48.3%;
                                                                                                                                                                                            14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1GCT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2200008D09RIK.
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                                                                                                                                                                                                                                                                                                                                                                                                             09CR35
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                                                                                                                                                                                                                                                                                                                                                              RESULT 7
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    SO RW
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                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
scrinopterygii; Neopterygii; Teleostei; Suteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
Pleuronectoidei; Paralichthyidae; Paralichthys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Suzuki T., Srivastava A.S., Kurokawa T.;
"Japanese flounder mRNA for chymotrypsinogen 1.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
EMBL; AB029753; BAA82365.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 261;
  Length 263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Archaea; Buryarchaeota; Methanococci; Methanosarcinales; Methanosarcinaceae; Methanosarcina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          D7090A9D65395B7D CRC64;
                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hydrogenase-3, subunit C (Hycc homolog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 35.8%; Score 59.5; DB 13; Best Local Similarity 48.5%; Pred. No. 3.8; Matches 16; Conservative 5; Mismatches 9;
     DB 11;
Score 71; DB 1:
Pred. No. 0.11;
                                                                                                                                                                                                                                                                                                                   261 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               648 AA
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InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00089; trypsin; 1.
SMARY; SM00020; Tryp_SPSI.
SMARY; SM00020; Tryp_SPS.; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
PROSITE; PS00135; TRYPSIN_SER; 1.
Hydrolase; Serine protease.
SEQUENCE 261 AA; 28184 MW; D7090A9D6539
                                                         5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MLLLSLTLSLVLLGSSWGCGVPAITPALS-YNQ 32
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MEDLINE-21929760; PubMed-11932238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chymotrypsinogen 1. Paralichthys olivaceus (Flounder).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
estinopterrygii; Neopterrygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
Pleuronectoidei; Paralichthyidae; Paralichthys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33.7%; Score 56; DB 13; Length 260; 45.0%; Pred. No. 11; tive 5; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27793 MW; 9F583044E22F78C0 CRC64;
                                                                                                                                                                                                                                                                                                                                                       InterPro; 1912;
InterPro; 1PR001254; Ser_protease_Try.
InterPro; 1PR001254; Ser_protease_Try.
Pfam; PF00089; trypsin; 1.
PRNINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_LIS; UNKNOWN_I.
PROSITE; PS00135; TRYPSIN_SER; 1.
Hydrolase; Serine protease.
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Best Local Similarity 38...
Local 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best_Local Similarity 45.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TrEMBLrel.
(TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  260 AA;
                                                                                                NCBI_TaxID=8255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gp21 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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096666
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Allen N., Naylor J., Stange-Thomann N., DeArellano K., Johnson R., Linton L., McEwan P., McKernan N., DeArellano K., Johnson R., Zimmer L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W., Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M. Hedderich R., Ingram-Smith C., Kuettner H.C., Krzycki J.A., Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K., Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C., Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E., Metonome of Macario B.;
                                                                                                                                                                                                                           "The genome of Methanosarcina acetivorans reveals extensive metabolic and physiological diversity."; Genome Res. 12:532-542(2002). EMBL; AE011156; AAM07710.1; -.
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InterPro; IPR000276; GPCR_Rhodpsn.
PROSTIE: PS0001; Trm_1; 1.
PROSTIE: PS00237; G_PROTEIN.RECEP_F1_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Vertebrata: Buteleostomi;
Vertebrata: Butherla: Primates: Catarrhini; Hominidae: Homo.
NCBI_TaxID=9606;
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216 216
216 AA, 23670 MW, 57E6534FB0B22C75 CRC64,
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01NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
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22.4%; Pred. No. 11;
iive 8; Mismatches
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Paralichthys olivaceus (Flounder).
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Best Local Similarity 60.0°
Matches 12; Conservative
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SEQUENCE 648 AA:
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Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
NCBI_TaxID=190478;
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                                                                                                                                                             SECUENCE FROM N.A.
Zimmer M., Scherer S., Loessner M.J.;
"Bacteriophage phi3626 complete genome.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY082070; AAL96791.1; --
SEQUENCE 140 AA; 15944 MW; 8D395E570A0A153C CRC64;
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Last annotation update)
3.
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21, Last sequence update)
21, Last annotation update)
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38.7%; Pred. No. /...
140 AA.
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SEQUENCE FROM N.A.
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Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
A manatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
A batton G.G., Wortman J.R., Yandrews Phannech M., Pfeiffer B.D.,
A hari J.F., Apbayani A., An H.-J., Andrews Pfannkoch C., Baldwin D.,
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Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
A borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
A de Pablos B., Detcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
A de Pablos B., Detcher M., Days A.D., Dew I., Dietz S.M.,
A de Pablos B., Detcher M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
Burtis K.C., Gabrielian A.E., Gorrell J.H., Gu Z., Guan P., Harris M.,
A Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
A Hostin D., Houston K.A., Howland T.J., Weil M.-H., Ibegwam C.,
Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
A Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
A Liu X., Mattei B., McIntosh T.C., McLeod M.P., Morberson D.,
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                                                                                                                                                               SEQUENCE FROM N.A.

Kawamura K., Shibata T., Saget O., Peel D., Shibata T., Bryant P.J.;

"A new family of growth factors produced by the fat body and active on brosophila imaginal disc cells.";

Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.

EMBL; AF102238; AAC99419.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                       SEQUENCE FROM N.A.

K., Shibata T., Peel D., Park S.-B., Bryant P.J.;
Kawamura K., Shibata T. Peel D., Park S.-B., Bryant P.J.;
Kolinase-related growth factors in Drosophila.";
Mol. Biol. Cell 8:358-358(1997).
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InterPro; IPR001223; Glyco.hydro_18.
Pfam; PF00704; Glyco.hydro_18; 1.
ProDom; PD000471; Glyco.hydro_18; 1.
SEQUENCE 441 Aa; 49219 MW; 988C297D09CA0B08 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNN-2002 (TrEMBLrel. 21, Last annotation update)
1DGF3 OR CG4559.
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Best Local Similarity
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                                                          NCBI_TaxID=7227;
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Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Nelson D.K., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Rese M.G.,
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
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Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
Milliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
R. F. J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zhao G.,
Cheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
The genome sequence of Drosophila melanogaster.";
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Ashburner M., Misra S., Roote J., Lewis S.E., Blazej R., Davis T.,
Doyle C., Galle R., George R., Harris M., Hartzell G., Harvey D.,
Hong L., Houston K., Hoskins R., Johnson G., Martin C., Moshrefi A.,
Palazzolo M., Reese M.G., Spradling A., Tsang G., Wan K., Whitelaw K.,
Celniker S., Rubin G.M.;
"An exploration of the sequence of a 2.9-Mb region of the genome of
Drosophila melanogaster: the Adh region.";
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Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.,
Yu C., Lewis S.E., Rubin G.M., Celniker S.;
Submitted (Jul-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AE003551; AAF535371;
EMBL; AE003416; AAF450181;
EMBL; AV047561; AAK77293.1;
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InterPro; IPR001223; Glyco_hydro_18.
Pfam; PF00704; Glyco_hydro_18; 1.
Propom; P000471; Glyco_hydro_18; 1.
SEQUENCE 441 AA; 49254 MW; F1938469FA117755 CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33.4%; Score 55.5; 48.3%; Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           210 LLLSLTV-LPNVNSSWYYDAPSLAF 237
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01-0CT-2001 (TrEMBLrel. 18, Last sequ
01-0CT-2001 (TrEMBLrel. 18, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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Matches 14; Conservative
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE TO STRAIN-ATCC 35092 / DSM 1617 / P2;

MEDINE-2132295; PubMed-11427726;

A bayez M.J., Chan-Welher C.C.-Y., Clausen I.G., Curtis B.A.,

A wayez M.J., Chan-Welher C.C.-Y., Clausen I.G., Curtis B.A.,

A be Moors A., Erauso G., Fletcher C., Gordon P.M.K.,

A helkamp-de Jong II., Jeffries A.C., Kozera C.J., Medina N., Peng X.,

A helkamp-de Jong II., Jeffries A.C., Kozera C.J., Medina N., Peng X.,

A helkamp-de Jong II., Defiries M.E., Theriault C., Tolstrup N.,

A charlebols R.L., Doollttle W.F., Duguet M., Gassterland T.,

A Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;

A The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";

Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).

REBL; AED06526; AAK41341.1;

RHYPOTHELICAL procedin; Complete proteome.

SCUENCE 835 AA; 92357 WW; BD28B5418BAF7250 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                    Sulfolobus solfataricus.
Archaea; Crenarchaeota; Thermoprotel; Sulfolobales; Sulfolobaceae;
Sulfolobus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 17; Length 835;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 33.4%; Score 55.5; Dest Local Similarity 44.8%; Pred. No. 40; Matches 13; Conservative 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search completed: December 20, 2002, 15:18:56 Job time : 6.08696 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MLLLSLTLSLV-----LLGSSWGCGVP 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 LLLLSLTLPIIPVNSQSTVVISSWGWGTP 37
Hypothetical protein SSO1079. SSO1079.
                                                                                                                       NCBI_TaxID=2287;
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GenCore version 5.1.3

Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 20, 2002, 15:12:58; Search time 1.13043 Seconds

(without alignments)

1210.790 Million cell updates/sec

Title: US-09-856-3198-4_COPY_1_33

Perfect score: 166
Sequence: 1 MLLLSLTLSLVLLGSSWGCGVPAITPALSYNOR 33

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
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Total number of hits satisfying chosen parameters: 112892

112892 seqs, 41476328 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		Description	homo	canis	P17538 homo sapien		Q96kk4 homo sapien	_	Q48465 klebsiella		084468 chlamydia t		-	P00164 trypanosoma		P06486 herpes simp	-	~	Q10644 mycobacteri	~	Q97ua2 sulfolobus	O95528 homo sapien	Q9ulz9 homo sapien	P00766 bos taurus	P00767 bos taurus	P47796 gadus morhu	Q91347 pseudomonas	P36142 saccharomyc	Q08274 mus musculu	P54484 bacillus su		•	~	Q56066 salmonella	Q8tmt1 methanosarc
SUMMARIES		di di	CTRL_HUMAN	CTR2_CANFA	CTRB_HUMAN	CTRB_RAT	OAC1_HUMAN	FL3L_MOUSE	MTGA_KLEPN	CLCR_HUMAN	ISPD_CHLTR	DF5L_HUMAN	MCT5_MOUSE	CYB_TRYBB	KM65_YEAST	US10_HSV11	VTU3_DROME	CPI9_SOLTU	YD33_MYCTU	MALX_KLEPN	PIP_SULSO	GT10_HUMAN ·	MM17_HUMAN	CTRA_BOVIN	CTRB_BOVIN	CTRA_GADMO	YG78_PSEAE	YK31_YEAST	DMWD_MOUSE	YQGA_BACSU	PAEP_HUMAN	ISPD_CHLMU	NU3M_STRCA	MOEA_SALTY	DNLI_METAC
		ength DB	264 1						242 1								119 1						606 1							142 1			116 1	m	568 1
đ	Query	Match Length	90.4	45.8	44.0	40.4	34.9	33.1	33.1	33.1	31.3	30.7	30.1	30.1	30.1	29.8	. 29.5	29.5	29.2	29.5	29.5	29.5	29.5	28.9	28.9	28.9	28.9	28.9	28.9	28.6	28.6	28.6	28.3	28.3	28.3
		Score	150	92	73	67	28	52	52	55	25	21	20	20	20	49.5	49	49	4	48.5	48:5	œ	48.5	48	48	48	48	48	4	7	7.	•	47	47	47
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P45582 asparagus o Q9um73 homo sapien P26847 marchantia P01150 rattus norv P24144 rhizobium 1 Q29461 bos taurus O63850 sarcophyton O24384 solanum tub P55091 rattus norv P24995 pisaster oc P97473 mus musculu
BGAL_ASPOF ALK_HUMAN NU3M_MARPO NU3M_MARPO NUDJ_RHILT REZ_BOVIN NU3M_SARGL CPIB_SOLTU CPIL_SOLTU CLCR RAT NUIM_PISOC TRBP_MOUSE
832 1620 118 255 262 269 117 222 222 268 3324
28 .3 28 .3 28 .0 28 .0 28 .0 27 .7 7 .7 7 .7 7 .7 7 .7 7 .7 7 .7
4444 64 44 644444 6666666666666
4 6 8 8 8 8 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9

## ALIGNMENTS

KESULT 1 CTRL_HUMAN	ı	01-FEB-1995 (Rel. 31, Creat 01-FEB-1995 (Rel. 31, Last	15-JUN-2002 (Rel. Chymotrypsin-like	sh CIRL OR CIRLI. OS Homo sapiens (Human).	Eukar	•	(1) SPORTENCE EDOM N &												DR EMBL; X71874; CAASO710.1;									DR PROSITE; PS00134; TRYPSIN_HIS; 1.	PROSITE; PS00135; TRYPSIN_SER; 1.			CHAIN 34 264 CHYMOTRYPSIN-LIKE PROTEA	ACT_SITE 75 75 CHARGE RELAY SYSTEM (BY	ACT_SITE 121	CARBOHYD 114 114 N-LINKED (GLUNAC ) (	DISULFID 19 141 BY SIMILARITY.	DISULFID 60 76 BY	FT DISULFID 155 220 BY SIMILARITY.	
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Best Local Similarity
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  Query Match
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                             Matches
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                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                      c. Natl. Acad. Sci. U.S.A. 80:7486-7490(1983).
CATALYTIC ACTIVITY: Preferential cleavage: Tyr-1-Xaa, Trp-1-Xaa,
                                                                                                                                                                                                                        13-A0G-1987 (Rel. 05, Created)
13-A0G-1987 (Rel. 05, Last sequence update)
15-A0W-1987 (Rel. 41, Last annotation update)
Chymotrypsinogen 2 precursor (EC 3.4.21.1).
Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-84170253; PubMed-6584866; Publsky S.D., Laforge K.S., Luc V., Scheele G.; Insky S.D., Laforge R.S., Luc V., Scheele G.; Identification of contact concess encoding secretory isoenzyme forms: sequence determination of canine pancreatic prechymotrypsinogen 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; A21195; A21195.

MEROPS; A21195.

MEROPS; S01.152.

InterPro; IPR011314; Chymotrypsin.

InterPro; IPR01254; Ser_protease_Try.

InterPro; IPR001254; Ser_protease_Try.

PRINTS; PR00722; CHYMOTRYPSIN.

SMART; SM00020; Tryp_SPC; 1.

PROSITE; PS00134; TRYPSIN_DOM; 1.

PROSITE; PS00134; TRYPSIN_SER; 1.

PROSITE; PS00135; TRYPSIN_SER; 1.

Hydrolase; Serine protease; Digestion; Pancreas; Zymogen; Signal.
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                                          Length 264;
                                                                      1; Indels
 BY SIMILARITY.
3F629F02FA6DDFB4 CRC64;
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CHYMOTRYPSIN 2, B CHAIN.
CHYMOTRYPSIN 2, C CHAIN.
CHARGE RELAY SYSTEM.
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CHARGE RELAY SYSTEM
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                                        Score 150; DB 1;
Pred. No. 2.5e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Phe-I'Xaa, Leu-I-Xaa.
-!- SUBCELLULAR LOCATION: EXTRACELLULAR.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.
                                                                                                                                                                                                  263 AA
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                                                                    3; Mismatches
                                                                                                                1 MLLLSLTLSLVLLGSSWGCGVPAITPALSYNOR 33
                                                                                                                                                                                                PRT;
           28002 MW;
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                                       90.48;
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210 :
264 AA;
                                                        Similarity
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P04813;
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                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: Preferential cleavage: Tyr-|-Xaa, Trp-|-Xaa,
                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                          Tomita N., Izumoto Y., Horil A., Doi S., Yokouchi H., Ogawa M., Mori T., Matsubara K.; "Molecular cloning and nucleotide sequence of human pancreatic prechymotrypsinogen cDNA.";
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45.8%; Score 76; DB 1; Length 263; 55.2%; Pred. No. 0.0085;
                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHYMOTRYPSIN B, A CHAIN.
CHYMOTRYPSIN B, B CHAIN.
CHYMOTRYPSIN B, C CHAIN.
CHARGE RELAY SYSTEM (BY SYCHARGE RELAY SYSTEM (BY SYCHARGE RELAY SYSTEM (BY S
                                10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last Sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-Strypsinogen B precursor (EC 3.4.21.1).
CTRB1 OR CTRB.
                                                                                                                                                                     263 AA.
                                3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Interpro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR001254; Ser_protease_Try.
PRIMTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPC; 1.
PR0SITE; PS50240; TRYPSIN_LOM; 1.
PROSITE; PS00134; TRYPSIN_LSE; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                              1 MLLLSLTLSLVLLGSSWGCGVPAITPALS 29
                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Pancreas;
MEDLINE=89134264; PubMed=2917002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; BC005385; AAH05385.1;
PIR; A31299; A31299.
HSSP; P00766; 1CHG.
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                                Conservative
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MIM; 118890; -.
                                                                                                                                                                     STANDARD;
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                                                                                                                                                                                                                                                                              Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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Gaps

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Indels

Score 67; DB 1; Length 263; Pred. No. 0.12;

Pred.

ACAFDBACF8C4DA6D CRC64;

BY SIMILARITY. BY SIMILARITY.

- Section

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5; Mismatches
                                                                                    1 MLLLSLTLSLVLLGSSWGCGVPAITPALS 29
                       27849 MW;
                                           40.48;
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                                                                13; Conservative
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                       263 AA;
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                                           Query Match
Best Local Similarity
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Q96KK4;
  DISULFID
DISULFID
SEQUENCE
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                                                                                                                                                                                                                                                                         Eukaryota; Métazoa; Chórdata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                          "Isolation and sequence of a rat chymotrypsin B gene.";
J. Biol. Chem. 259:14265-14270(1984).
-!- CATALYTIC ACTIVITY: Preferential cleavage: Tyr-|-Xaa, Trp-|-Xaa,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHYMOTRYPSINOGEN B.
CHYMOTRYPSINOGEN B. A CHAIN.
CHYMOTRYPSIN B. A CHAIN.
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SMART; SW00020; TYP_SPC; 1.
PROSITE; PSSO0134; TRYPSIN_LDOM; 1.
PROSITE; PS00134; TRYPSIN_LIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
Hydrolase; Serine protease; Digestion; Pancreas; Zymogen; Signal.
                                                                                              ;
                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDILNE-88054881: PubMed-6209274;
Bell G.I., Quinto C., Quiroga M., Valenzuela P., Craik C.S.,
Rutter W.J.;
                                                                     Score 73; DB 1; Length 263;
Pred. No. 0.021;
                                                                                             10; Indels
BY SIMILARITY.
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ACICO55A490B8701 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                         Phe-I-Xaa, Leu-I-Xaa.
-!- SUBCELLULAR LOCATION: Extracellular.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.
                                                                                                                                                                                                            01-APR-1988 (Rel. 07, Created)
01-APR-1988 (Rel. 07, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Chymotrypsinogen B precursor (EC 3.4.21.1).
                                                                                                                                                                                          263 AA
                                                                                             3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
                                                                                                                1 MLLLSLTLSLVLLGSSWGCGVPAITPALS 29
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  140 B3 76 B3 219 B3 200 B3 238 B3 27870 MW;
                                                                       ch 44.0%;
1 Similarity 55.2%;
16; Conservative :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00089; trypsin; 1
                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
                               186 2
209 2
263 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; A22658; KYRTB.
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                                                                                  Best Local Similarity
Matches 16; Conserv
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                   DISULFID
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SEQUENCE
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CTRB_RAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -: SUBCELLUIAR LOCATION: Integral membrane protein -: SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ·LINKED (GLCNAC. . .) (POTENTIAL).
B6FD6E0E700CB2CC CRC64;
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InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Multigene family; Olfaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Whitaker H.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PUTATIVE ODORANT RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                  15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Olfactory receptor 10c1 (Hs6M1-17).
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2; Mismatches
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34351 MW;
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RESULT 7
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MEDLINE-94064/791; PubMed=7505204;
Lyman S.D., James L., Vandenbos T., Devries P., Brasel K.,
Lyman S.D., James L., Vandenbos T., Devries P., McKenna H.J.,
Glinlak B., Hollingsworth L.T., Picha K.S., McKenna H.J.,
Splett R.R., Fletcher F.A., Maraskovsky E., Farrah T.,
Foxworthe D., Williams D.E., Beckmann M.P.;
Molecular cloning of a ligand for the fil3/fik-2 tyrosine kinase
receptor: a proliferative factor for primitive hematopoletic cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Type I membrane protein. Two soluble isoforms are also produced by alternative splicing. One of which, isoform 3/E6, is biologically active, while the other, isoform 4/E6Deltal6, is inactive.

ALTERNATIVE PRODUCTS: 4 isoforms; 1/6C (shown here), 2/5H, 3/E6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Identification of soluble and membrane-bound isoforms of the murine flt3 ligand generated by alternative splicing of mRNAs."; Oncogene 10:149-157(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    McClanahan T., Culpepper J., Campbell D., Wagner J., Franz-Bacon K., Mattson J., Tsai S., Luh J., Guimares M.J., Mattel M.-G., Rosnet O., Birnbaum D., Hannum C.; Submitted (Apr-1965) to the EMBL/GenBank/PDBJ databases.
-!- FUNCTION: STIMULATES THE PROLIFERATION OF EARLY HEMATOPOLETIC CELLS. SYNERGIZES WELL WITH A NUMBER OF OTHER COLONY STIMULATING FACTORS AND INTERLEUKINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Structural analysis of human and murine flt3 ligand genomic loci."; Oncogene 11:1165-1172(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

MEDLINE-94195428; PubMed-8145851;
Hannum C., Culpepper J., Campbell D., McClanahan T., Zurawski S.,
Bazan J.F., Kastelein R., Hudak S., Wagner J., Mattson J., Luh J.,
Buda G., Martina N., Peterson D., Menon S., Shanafelt A.,
Muench M., Kelner G., Namikawa R., Rennick D., Roncarolo M.G.,
Zlotnik A., Rosnet O., Dubreuil P., Birnbaum D., Lee F.;
Higand for FUJYFLKZ receptor tyrosine kinase regulates growth of haemstopoletic stem cells and is encoded by variant RNAS.";
Nature 368:643-648(1994).
                                                                                                                                             FL3L_MOUSE STANDARD; PRT; 232 AA.
P49772; 064085;
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
SL cytokine precursor (Fms-related tyrosine kinase 3 ligand) (Flt3)
                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lyman S.D., Stocking K., Davison B., Fletcher F., Johnson L.,
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С
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MEDILINE-95124710; Pubmed-782427;
L., James L., Escobar S., Downey H., de Vries
Brasel K., Stocking K., Beckmann M.P., Copeland N.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
MEDLINE-96032581; PubMed-7566977;
                    LLLSHRVCLQLAGSAWACGV 152
                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                    ligand) (Flt3L)
FLT3LG OR FLT3L
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                    133
                                                                                                RESULT 6
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SL CYTOKINE.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
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BY SIMILARITY.
N'LINKED (GLCNAC. . .) (POTENTIAL).
N'LINKED (GLCNAC. . .) (POTENTIAL).
N'LINKED (GLCNAC. . .) (POTENTIAL).
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HGATRLTATALLTVCPGLLLPLVGTSHMFFLPYFLSFLSSF
LKMYLYV (IN ISOFORM 2).
BSSTLL -> GSHYAG (IN ISOFORM 3).
MISSING (IN ISOFORM 3).
VQCQP -> GLIMQARLTLNSKQSSCLSVLSAGIT (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                       Cytokine; Glycoprotein; Transmembrane; Alternative splicing; Signal SIGNAL 1 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Spratt B.G., Zhou J., Taylor M., Merrick M.J.;
"Monofunctional biosynthetic peptidoglycan transglycosylases.";
Mol. Microbiol. 19:639-640(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Monofunctional biosyphthetic peptidoglycan transglycosylase (EC 2.4.2..) (Monofunctional TGase).
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MISSING (IN REF. 2).
3A3680D3CB69FBA6 CRC64;
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MEDLINE=96228711; PubMed=8830253;
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InterPro; IPR004213; Flt3_lig.
Pfam; PF02947; flt3_lig; 1.
                                                                                                                                                                                  123636, AAA39436.1; ... 129875; AAA90951.1; ... 129875; AAA90952.1; ... 576459; AAB33070.1; ... 576461; AAB33070.1; ... 576464; AAB33071.1; ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26141 MW;
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61.1%;
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193 LLLLLLPLTLVLLAAAWG 210
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232 AA;
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Matches 11; Conserv
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                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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its homologue, elastase IV, is an artifact during cloning derived
from caldecrin gene.";
J. Blochem. 123:546-554(1998).
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                                                                                                                                                                                                                                                                         Gaps
   PATHWAY: FINAL STAGES IN PEPTIDOGLYCAN SYNTHESIS.
SUBCELLULAR LOCATION: Membrane-associated (Potential).
SIMILARITY: TO THE N-TERMINAL OF BACTERIAL CLASS IA PENICILLIN-BINDING PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yoshino-Yasuda I., Kobayashi K., Akiyama M., Itoh H., Tomomura A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
                                                                                                                                                                           Pfam: PF00312; TransglyGosyl; 1.
ProDom: PD001895; GT 51; 1.
Protom: Pp001895; GT 51; 1.
TRANSMEM 19 39 POTENTIAL.
SEQUENCE 242 AA; 27196 MW; A12CAB4A331ABA49 CRC64;
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"A human pancreatic chymotrypsin: biochemical and molecular
characterization.";
                                                                                                                                                                                                                                               33.1%; Score 55; DB 1; Length 242; 58.8%; Pred. No. 4; 1.1ve 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Molecular cloning and expression of human caldecrin."; FEBS Lett. 386:26-28(1996).
                                                                                                                                                                                                                                                                                                                                                                         CLCR_HUMAN STANDARD, PRT; 268 AA. 99895; Q9NUH5; O00765; G9T 2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) calderin precursor (EC 3.4.21.2) (Chymotrypsin C).
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TISSUE-Pancreas;
FUNCTION: CELL WALL FORMATION
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MEDLINE-98207038; Pubmed-9538241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 17-268 FROM N.A.
                                                                                                                                                                    InterPro; IPR001264; GT_51.
                                                                                                                                                                                                                                                                                                           EMBL; 254198; CAA90903.1;
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                                                                                                                                                                                                                                                          Best Local Similarity 58.8
Matches 10; Conservative
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Homo sapiens (Human).
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30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase (EC 2.7.7.60)
(4-diphosphocytidyl-2C-methyl-D-erythritol synthase) (MEP
cytidylyltransferase) (MCT).
Cytidylyltransferase) (MCT).
Chlamydia trachomatis.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
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CATALYTIC ACTIVITY: Preferential cleavage: Leu-|-Xaa, Tyr-|-Xaa,
                               Phe-|-Xaa, Met-|-Xaa, Trp-|-Xaa, Gln-|-Xaa, Asn-|-Xaa.
-|- TISSUE SPECIFICITY: PANCREAS.
-|- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. ELASTASE SUBFAMILY.
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-> D (IN REF. 3)
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InterPro; IPR001254; Ser_protease_Try.
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EMBL; AL031283; CAB77355.1; -.
EMBL; Y13697; CAB74031.1; -.
HSSP; P00766; LCHG.
MEROPS; S01.157; -.
Genew; HGNC:2523; CTRC.
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PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_HIS; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-92287966; Pubmed-1376147;
Chu W., Johnson D.A., Musich P.R.;
"Molecular cloning and characterization of mouse mast cell chymases.";
Biochim. Biophys. Acta 1121:83-87(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MCNeil H.P., Austen K.F., Somerville L.L., Gurish M.F., Stevens R.L.; Molecular cloning of the mouse mast cell protease-5 gene. A novel secretory granule protease expressed early in the differentiation of serosal mast cells.";
J. Biol. Chem. 266:20316-20322(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Huang R., Blom T., Hellman L.; "Cloning and structural analysis of MMCP-1, MMCP-4 and MMCP-5, three mouse mast cell-specific serine proteases."; Eur. J. Immunol. 21:1611-1621(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-92407343; PubMed-1527387; McNeil H.P., Frenkel D.P., Austen F., Friend D.S., Stevens R.L.; Translation and granule localization of mouse mast cell protease-5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Different mouse mast cell populations express various combinations of at least six distinct mast cell serine proteases."; Proc. Natl. Acad. Sci. U.S.A. 87:3230-3234(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-1991 (Rel. 18, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Mast cell protease 5 precursor (EC 3.4.21.-) (MMCP-5) (Mast cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 22-51.
MEDLINE=90222202; PubMed=2326280;
Reynolds D.S., Stevens R.L., Lane W.S., Carr M.H., Austen K.F.,
Serafin W.E.;
                                                                                                                                                                                                                                                                                                                                                                              30.7%; Score 51; DB 1; Length 484; 63.2%; Pred. No. 24; ive 2; Mismatches 3; Indels
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
-! SIMILARITY: BELONGS TO THE DFN5 FAMILY.
                                                                                                                                                                                                                                                                           EMBL; AK022212; BAB13986.1; -.
EMBL; BC008904; AAH08904.1; -.
SEQUENCE 484 AA; 52801 MW; F7CE8073E0C0194D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN-Leaden X A1; TISSUE-Connective tissue; STRAIN-Leaden X A1; TISSUE-Connective tissue; MEDLINE-91285010; PUMM04-2060576;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        247 AA
                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE-92041862; Pubmed=1939089;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          420 TMSLPPGLLGNSWGEGAPA 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 TLSLV--LLGSSWGCGVPA 23
                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 63.2
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chymase 1).
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P21844;
                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L., Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
                                                                                                                                                                                                                              Chlamydia frachomatis.";
Science 283:754-759(1998).
-!- FUNCTION: CATALYZES THE FORMATION OF 4-DIPHOSPHOCYTIDYL-2C-METHYL-
                                                                                                                                                                                                                                                                                                                                                         -1- CATALYTIC ACTIVITY: CTP + 2-C-methyl-D-erythritol 4-phosphate = diphosphate + 4-(cytidine 5'-diphospho) -2-C-methyl-D-erythritol.
-1- PATHWAY: Nonmevalonate terpenoid biosynthesis pathway; third step.
-1- SIMILARITY: BELONGS TO THE ISPD FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

TISSUB-Mammary gland;

TISSUB-Mammary gland;

TISSUB-Mammary gland;

TISSUB-Mammary gland;

TISSUB-Mammary gland;

Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,

Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,

Takahashi M., Oliba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,

Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,

Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,

NINOMIYA K., Itayanagi T.;

"NEDO human cDNA sequencing project.";

Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                         D-ERYTHRITOL FROM CTP AND 2C-METHYL-D-ERYTHRITOL 4-PHOSPHATE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Primates; Catarrhini, Hominidae; Homo.
                                                                                                                                                                                                      "Genome sequence of an obligate intracellular pathogen of humans:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transferase; Nucleotidyltransferase; Isoprene biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 31.3%; Score 52; DB 1; Length 219; I Similarity 36.4%; Pred. No. 8.8; 16; Conservative 3; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              219 AA; 24168 MW; 45C69BF82505364D CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-ocr-2001 (Rel. 40, Created)
16-ocr-2001 (Rel. 40, Last sequence update)
15-UNY-2002 (Rel. 41, Last annotation update)
DFNS-like protein FLJ12150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       484 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPR001228; ISPD_synthase.
                                                                             STRAIN=D/UW-3/Cx;
MEDLINE-99000809; PubMed-9784136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE001320; AAC68062.1; -. HSSP; Q46893; 11NJ.
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PROSITE; PS01295; ISPD; 1.
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Best Local Similarity
                                [1]
SEQUENCE FROM N.A.
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  NCBI_TaxID=813;
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Strausberg R.;
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P57764;
                                                                                                                                                                                Davis R.W.
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DF5L_HUMAN

RESULT 10

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Matches

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KM65_YEAST
Q03656;
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      RRTH RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY RESERVED BY R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                J. Immunol. 149:2466-2472(1992).
-!- SUBCELLULAR LOCATION: Secretory granules.
-!- TISSUE SPECIFICITY: MAST CELLS.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. GRANZYME SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
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N-LINKED (GLCNAC. .) (POTENTIAL).
T -> A (IN REF. 1).
C -> R (IN REF. 4).
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Pred. No. 18;
5; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glycoprotein; Zymogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24C290CF61237DC7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-84041494; PubMed-6314266;
Benne R., de Vries B.F., van den Burg J., Klaver B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACTIVATION PEPTIDE. MAST CELL PROTEASE
Immunodetection with specific antipeptide Ig.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MLLLSLTLSLVLLGSSWGCG-----VPAITPALSY 30
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21-JUL-1986 (Rel. 01, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
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InterPro: IPR001314; Chymotrypsin.
InterPro: IPR001254; Ser_protease_Try.
Pfam; PF00089; trypsin: 1.
PR00712; CHYMOTRYPSIN.
SWART; SW00020; Tryp_SPC: 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00135; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
HydroLase; Serie protease; Signal; Glycol SIGNAL
                                                                                                                                                                                                                                                                      EMBL; X68805; CAA48705.1; ALT_INIT.
EMBL; M73759; AAA40105.1; -.
EMBL; M73760; -; NOT_ANNOTATED_CDS.
EMBL; M68898; AAA33492.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27586 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30.1%;
Local Similarity 39.5%;
hes 15; Conservative 5
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                                                                                                                                                                                                                                                                                                                                                                                                                             MGD; MGI:96941; Mcpt5.
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PIR; C35646; C35646.
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224
247 AA;
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MEROPS; S01.150; -.
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P00164;
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ACT_SITE
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SEQUENCE
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Matches
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CYB_TRYBB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
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                                                                                                                                                                                                                                         COUPLED TO ATP SYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000179; Cyt_b_b6.
InterPro; IPR001230; Prenyl_site.
Pfam: PF000132; Cytochrome_b_C; I.
Pfam: PF00033; Cytochrome_b_N; I.
PROSTER; PS00192; CYTOCHROME_B_HEME; I.
PROSTER; PS00193; CYTOCHROME_B_D; D: I.
Electron transport; Mitochondrion; Respiratory chain; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
"The nucleotide sequence of a segment of Trypanosoma brucei mitochondrial maxi-circle DNA that contains the gene for apocytochrome b and some unual unassigned reading frames."; Nucleic Acids Res. 11:6925-6941(1983).
-!- FUNKTION: COMPONENT OF THE UBIGGINOL-CYTOCHROME C REDUCTASE COMPLEX (COMPLEX LII OR CYTOCHROME B-C1 COMPLEX), WHICH IS A RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
                                                                                                                                                                                                                                                                                                                 BOUND TO THE PROTEIN.
-!- SUBUNTY: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B, CYTOCHROME C1 AND THE RIESKE PROTEIN.
-!- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
SIMILAR TO S.POMBE DSK1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Fungi, Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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01-NOV-1997 (Rel. 35, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Probable serine/threonine-protein kinase YMR216C (EC 2.7.1.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-S288c / AB972;
Dedman K., Brown D., Bowman S., Barrell B.G., Rajandream M.A.,
Walsh S.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IRON 1 (HEME B562 AXIAL LIGAND)
IRON 2 (HEME B566 AXIAL LIGAND)
IRON 2 (HEME B562 AXIAL LIGAND)
IRON 1 (HEME B566 AXIAL LIGAND)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30.1%; Score 50; DB 1; Length 363; 46.4%; Pred. No. 25; tive 3; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2A37CD827E55923B CRC64;
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88
175
189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 363 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
nes 13; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Heme; Kinetoplast
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PIR; A05242; QQBE07
                                                                                                                                                                                                                               VTU3_DROME
                                                                      SEQUENCE
                                                                                               Query Match
                                                           ZN_FING
                                                                                                          Best Local
Matches
                                                                                                                                                                                                       RESULT 15
VTU3_DROME
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                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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  and for commercial
            entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rixon F.J., McGeoch D.J.;
"A 3' co-terminal family of mRNAs from the herpes simplex virus type
1 short region: two overlapping reading frames encode unrelated
polypeptide one of which has highly reiterated amino acid sequence.";
Nucleic Acids Res. 12:2473-2487(1984).
-!- SIMILARITY: BELONGS TO A FAMILY THAT GROUP TOGETHER HSV-1 US10,
EHV-1 66, EHV-4 ORF3, AND VZV 64/69.
                                                                                                                                                                                                                                                                            Gaps
                                           EMBL; Z49809; CAA89931.1; -.
SGD; S0004829; YMR216C.
InterPro; IPR000719; EUK_pkinase.
Pfam: PF00069; pkinase; 1.
ProDom; PD000001; EUK_pkinase; 2.
PROSITE; PS001007; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00108; PROTEIN_KINASE_BOM; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
Hypothetical protein; Transferase; Serine/threonine-protein kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=85160822; PubMed=2984429;
McGeoch D.J., Dolan A., Donald S., Rixon F.J.;
"Sequence determination and genetic content of the short unique region in the genome of herpes simplex virus type 1.";
J. Mol. Biol. 181:1-13(1985).
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                                                                                                                                                                                                                                                   30.1%; Score 50; DB 1; Length 742; 80.0%; Pred. No. 49;
                                                                                                                                                                                                                                                                            1; Indels
  Usage by
                                                                                                                                                                                                                BY SIMILARITY.
C775F10B30C950FC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Herpes simplex virus (type 1 / strain 17).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Apphaherpesvirinae; Simplexvirus.
NCBI_TaxID=10299;
                                                                                                                                                                                         ATP (BY SIMILARITY). ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                       01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
01-ARR-1993 (Rel. 25, Last annotation update)
Virion protein US10.
modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                    312 AA.
                                                                                                                                                                               PROTEIN KINASE
                                                                                                                                                                                                                                                                            1; Mismatches
                        send an email to license@isb-sib.ch).
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MEDLINE=84169548; PubMed=6324121;
                                                                                                                                                                                                                             83237 MW;
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                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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164
187
294
742 AA;
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575 VLLGAPWGCG 584
                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                  11 VLLGSSWGCG 20
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8
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SEQUENCE
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BINDING
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                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Scherer L.J., Harris D.H., Petri W.H.;

"Drosophila vitelline membrane genes contain a 114 base pair region
"Drosophila vitelline membrane genes contain a 114 base pair region
of highly conserved coding sequence.";
Dev. Biol. 130:786-788(1988).
-!- FUNCTION: MAJONE EARLY EGGSHELL PROTEIN.
-!- FUNCTION: MAJONE EARLY EGGSHELL CELLS.
-!- TISSUE SPECIFICITY: FOLLICLE CELLS.
-!- DEVELOPMENTAL STAGE: EXPRESSED DURING VITELLINE MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: A 38 AMINO ACIDS REGION (VM DOMAIN) IS CONSERVED IN DROSOPHILA VITELLINE MEMBRANE PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Isolation and chromosomal location of putative vitelline membrane genes in Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-Daekwanryeong;
MEDLINE-82257433; Pubmed-3926479;
Mindrinos M.N., Scherer L.J., Garcini F.J., Kwan H., Jacobs K.A.,
                                                                                                                                                                                                                                                  DB 1; Length 312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Scherer L.J., Harris D.H., White M.K., Steel L.S., Jin J.,
                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                            POTENTIAL.
12D01B0E7C920EA3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-0cT-1996 (Rel. 34, Created)
01-0cT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
WM34CA OR WM34C.1.
                                                                                                                                                                                                                             / match 29.8%; Score 49.5; 1 Local Similarity 54.5%; Pred. No. 26; les 12; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=94123988; PubMed=8293994;
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MEDLINE=89065296; PubMed=3143615;
                                                                                                                                                                                                                                                                                                                                                                                                                           291 THCLHLFG-AFGCGDPALTPPL 311
InterPro; IPR000087; Collagen.
InterPro; IPR000714; EHV_Unk.
Pfam; PF02053; Gene66; 1.
                                                                                                                                                                                                                                                                                                                                                                                    7 TLSLVLLGSSWGCGVPAITPAL 28
                                                                                                                                                293 E
34055 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-96 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBO J. 4:147-153(1985).
                                                                                                                                            271
312 AA;
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DR EMBL; M22700; AAA29018.1; -.
DR FlyBase; FBgn0003983; vm34ca.
KW Signal; Structural protein; Eggshell.
FT SIGNAL
1 1 9 VITELLINE MEMBRANE PROTEIN VM34CA.
FT CHAIN 20 119 VITELLINE MEMBRANE PROTEIN VM34CA.
FT CONFLICT 96 96 A -> Main No.
FT CONFLICT 96 96 A -> FT CONFLICT 96 96 Best Local Similarity 54.5%; Pred. No. 12;

Query Match
0uery Match
12 LLGSSW-GCGVPAITPALSYN 31
11|1: | | | | | | | |
Db 25 MLGSSYGGGYGRPAAPAPSYS 46
Search completed: December 20, 2002, 15:17:14
Job time: 2.13043 secs
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GenCore version 5.1.3
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OM protein - protein search, using sw model

December 20, 2002, 15:16:49; Search time 8.34783 Seconds (without alignments) 530.147 Million cell updates/sec Run on:

US-09-856-319B-4 1418 1 MLLLSLTLSLVLLGSSWGCG......AMYTRVSKFSTWINQVMAXN 264 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

106657 seqs, 16763532 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

Published_Applications_AA:*

1: /cgn2_6/ptodata/1/pupaa/US08_NEW_PUB.pep:*
2: /cgn2_6/ptodata/1/pupaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/puppaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/puppaa/US06_NEW_PUB.pep:*
5: /cgn2_6/ptodata/1/puppaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US00_PUBCOMB.pep:*

10: 11: 12: 14:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	D Description	US-09-925-297-529 Sequence 529, App	US-09-888-615-96 Sequence 96, Appl	JS-09-335-325-1 Sequence 1, Appli	-1 Sequence 1	-		^,	695	S	US-09-946-893-2 Sequence 2, Appli	6	Sequence 69,	JS-09-978-192A-69 Sequence 69, Appl	US-10-052-586-64 Sequence 64, Appl	17		Sequence 8,	US-09-888-615-103 Seguence 103. App	
	DB I	10	10	0 6	10	10	10	10	10	n 6	10	D 6	n 6	n 6	12	10	10	10	10	
	Query Match Length DB	192	263	812	812	812	812	270	273	791	810	453	453	453	453	248	327	327	454	
œ	Query Match 1	62.7	58.0	34.2	34.2	34.2	34.2	34.2	34.2	34.1	34.1	33.0	33.0	33.0	33.0	33.0	33:0	33.0	33.0	0
	Score	889	822.5	485.5	485.5	485.5	485.5	484.5	484.5	484	484	468.5	468.5	468.5	468.5	468	468	468	468	
	Result No.	-	7	m	4	S	9	7	80	6	10	11	12	13	14	15	16	17	18	,

Sequence 2, Appl1 Sequence 5, Appl1 Sequence 6, Appl1 Sequence 5, Appl1 Sequence 126, Appl Sequence 934, App Sequence 934, App Sequence 934, App Sequence 934, App Sequence 934, App Sequence 931, App Sequence 931, App Sequence 931, App Sequence 932, App Sequence 932, App	Sequence 895, App Sequence 895, App Sequence 14, Appl Sequence 14, Appl Sequence 23, Appl Sequence 101, Appl Sequence 90, Appl Sequence 7, Appl1 Sequence 7, Appl1 Sequence 7, Appl1
10 US-09-948-094-2 9 US-09-961-721-6 9 US-09-961-721-6 9 US-09-961-721-6 10 US-09-910-151-6 9 US-09-910-151-6 9 US-09-910-151-6 9 US-09-759-126 9 US-09-759-143-934 10 US-09-759-143-934 10 US-09-759-143-934 10 US-09-759-143-934 10 US-09-759-143-934 10 US-09-759-143-934 10 US-09-759-143-932 10 US-09-759-143-932 10 US-09-759-143-932	9 US-10-012-896-895 10 US-09-759-143-895 10 US-09-789-143-895 10 US-09-879-792-14 0 US-09-812-895 10 US-09-813-23 10 US-09-888-615-101 10 US-09-888-615-90 12 US-10-041-264A-7 12 US-10-042-091A-7 12 US-10-042-091A-7 10 US-09-988-975A-1
222 2226 2226 2226 3329 3329 4292 4292 4292 4292 4292	44444 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 900000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 900000 90000 90000 90000 90000 90000 90000 90000 90000 900000 90000 90000 90000 90000 90000 90000 90000 90000 900000 90000 90000 90000 90000 90000 90000 90000 90000 900000 90000 90000 90000 90000 90000 90000 90000 90000 900000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 900000 90000 90000 90000 90000 90000 90000 90000 90000 900000 90000 90000 90000 90000 90000 90000 90000 90000 900000 90000 90000 90000 90000 90000 90000 90000 90000 900000 90000 90000 90000 90000 90000 90000 90000 90000 900000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000 90000
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200 200 200 200 300 330 330	8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8

## ALIGNMENTS

APPLICANT: Rosen et al.
TITLE OFE INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PAIO5
CURRENT APPLICATION NUMBER: US/09/925,297
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/USO0/05989
PRIOR PELING DATE: 2000-03-08
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 928
SOFTWARE: PATENTIN VET: 2.0
SEQ ID NOS: 928
LENGTH: 192
TYPE: PRT Sequence 529, Application US/09925297 Patent No. US20020081659A1 ; ORGANISM: Homo sapiens US-09-925-297-529 GENERAL INFORMATION: us-09-925-297-529

Gaps ö Length 192; 62.7%; Score 889; DB 10; Length 1 84.7%; Pred. No. 1e-71; Live 19; Mismatches 10; Indels Best Local Similarity 84.7 Matches 160; Conservative Query Match Best Local Similarity

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65 ISPNWVVTAAHCQVTPGRHFVVLGEYDRSSNAEPVQVLSIARAITHPNWNANTMNNDLTL 124 g ò g

5 SLTLSLVLLGSSWGCGVPAITPALSYNQRIVNGENAVPGSWPWQVSLQDNTGFHFCGGSL

125 LKLASPARYTAQVSPVCLASTNEALPSGLTCVTTGWGRISGVGNVTPARLQQVVLPLVTV 184 à QQ

185 NQCROYWGA 193 셤 ò

181 NQCRQYWGS 189

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557 IPLCASASSFECGKPQVEPK-KCPGRVVGGCVANPHSWPWQISLRTRFTGQHFCGGTLIA 615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67 PNWVVTAAHC---QVTPGRHFVVLGEYDRSSNAEPVQVLSIARAITHPNWNANTMNNDLT 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              O'Reilly, Michael
TITLE OF INVENTION: Angiostatin Fragments and Method of Use
UNUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 191 Peachtree Street, 37th Floor CITY: Atlanta STATE: Georgia COUNTRY: USA ZIP: 30303-1769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 34.2%; Score 485.5; DB 9; Best Local Similarity 40.0%; Pred. No. 2.9e-35; Matches 106; Conservative 35; Mismatches 107;
                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/612,788
FILING DATE: <UNKNOWN>
ATTORNEY,AGENT INFORMATION:
NAME: Warren, William L.
REGISTRATION NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 05213-0126
                                  APPLICATION NUMBER: US/09/335,325
FILING DATE: 17-Jun-1999
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLONE: Plasminogen
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jones & Askew, LLP
                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-818-3700
TELEFAX: 404-818-3799
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 812 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             240 NIQAPAMYTRVSKFSTWINQVMAYN 264
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Patent No. US20010029246A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Folkman, M. Judah
                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: <Unknown>
                    CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANTI-SENSE: NO FRAGMENT TYPE: N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Murine
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
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US-09-788-142-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 DLTLLKLASPARYTAQVSPVCLASTNEALPSGLTCVTTGWGRISGVGNVTPARLQQVVLP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 LVTVNQCRQYWGARITDAMICAGGSGASSCQGDSGGPLVCQKGNTWVLIGIVSWGTKNCN 240
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Cao, Yihai
Sim, B. Kim Lee
TITLE OF INVENTION: Angiostatin Fragments and Method of Use
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 263;
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nes 73; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Pred. No. 1.1e 39; Mismatches
                                                                                                                                          APPLICANT: WHYTE, DAVID
APPLICANT: WHYTE, DAVID
APPLICANT: CARNEPEEL, SEAN
APPLICANT: CARNEPEEL, SEAN
APPLICANT: CARNEPEEL, SEAN
APPLICANT: MANNING, GERRED
TITLE OF INVENTION: NOVEL PROTEASES
FILE REFERENCE: 038602/1214
CURRENT APPLICATION NUMBER: US/09/88,615
CURRENT FILING DATE: 2001-06-26
PRIOR FILING DATE: 2000-06-26
NUMBER OF SEQ ID NOS: 150
SOFTWARE: PATENTING DATE: 2000-06-26
NUMBER OF SEQ ID NOS: 150
SOFTWARE: PATENTING DATE: 2000-06-26
NUMBER OF SEQ ID NOS: 150
SOFTWARE: PATENTING DATE: 2000-06-26
NUMBER OF SEQ ID NOS: 150
SOFTWARE: PATENTING DATE: 2000-06-26
LENGTH: 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 822.5;
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ZIP: 3030-1769
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                            Sequence 96, Application US/0988615
Patent No. US20020064856A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 IQAPAMYTRVSKFSTWINQVMAYN 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     240 TTTPAVYARVTKLIPWVQKILAAN 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/0933535
Patent No. US20020164717A1
GENERAL INFORMATION:
APPLICANT: Folkman, M. Judah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 58.0%;
Best Local Similarity 57.2%;
Matches 151; Conservative 3
                                                                                                                                 APPLICANT: PLOWMAN, GREGORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
US-09-888-615-96
                                                                                                     GENERAL INFORMATION:
                                         US-09-888-615-96
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Gaps

Indels 17;

Length 812;

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Sequence 81, Application US/09873676

Betent No. US20020077289A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: MacDonald, Nicholas J.

APPLICANT: Sim, Kim L.

TITLE OF INVERTION: Anglostatin and Endostatin Binding Proteins and Methods of Use
FILE REFERENCE: 05213-0378 (43170-259333)

CURRENT APPLICATION NUMBER: US/09/873,676

CURRENT FILING DATE: 2001-06-04

PRIOR FILING DATE: 2000-06-02

PRIOR FILING DATE: 2001-06-09

PRIOR FILING DATE: 2001-06-00

PRIOR FILING DATE: 2001-06-00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LLKLASPARYTAQVSPVCLASTNEALPSGLTCVTTGWGRISGVGNVTPARLQQVVLPLVT 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             184 VNQCR--QYWGARITDAMICAG--GSGASSCQGDSGGPLVCQKGNTWVLIGIVSWGTKNC 239
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                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                            8 LSLVLLGSSWGCGVPAITPALSYNQRIVNGENAVPGSWPWQVSLQDN-TGFHFCGGSLIS 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 LSLVLLGSSWGCGVPAITPALSYNQRIVNGENAVPGSWPWQVSLQDN-TGFHFCGGSLIS 66
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                                                                                                                                                                                                                                                                                                                                   Length 812;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 34.2%; Score 485.5; DB 10; Length 9 Best Local Similarity 40.0%; Pred. No. 2.9e-35; Matches 106; Conservative 35; Mismatches 107; Indels
                                                                                                                                                                                                                                                                                                                              34.2%; Score 485.5; DB 10; Length 40.0%; Pred. No. 2.9e-35; tive 35; Mismatches 107; Indels
PRIOR FILING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 08/666,735
PRIOR FILING DATE: 1997-05-30
NUMBER OF SEQ ID NOS: 47
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 240 NIQAPAMYTRVSKFSTWINQVMAYN 264
                                                                                                                                                                                                                                NAME/KEY: misc_feature; OTHER INFORMATION: Plasminogen US-09-761-120-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 123
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 40.0%
Matches 106; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Murinae gen. sp. US-09-873-676-81
                                                                                                                                         LENGTH: 812
TYPE: PRT
ORGANISM: Murinae gen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-873-676-81
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                                                                                                                      SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
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APPLICANT: FOLKman, M. Judah
APPLICANT: FOLKman, M. Judah
APPLICANT: FOLKman, M. Judah
APPLICANT: O'Really, Michael
APPLICANT: O'Really, Michael
FILE REFERENCE: 05940-0151 (43171-252068)
CURRENT FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: 09/309,821
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       670 LLKLSRPATITDKVIPACLPSPNYMVADRTICYITGWGETQGTFGA--GRLKEAQLPVIE 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 LSLVLLGSSWGCGVPAITPALSYNQRIVNGENAVPGSWPWQVSLQDN-TGFHFCGGSLIS 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  184 VNQCR--QYWGARITDAMICAG--GSGASSCQGDSGGPLVCQKGNTWVLIGIVSWGTKNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 812;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34.2%; Score 485.5; DB 10; Length 40.0%; Pred. No. 2.9e-35; tive 35; Mismatches 107; Indels
                                    COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/788,142
FILING DATE: 16-Feb-2001
CLASSIFICATION: <u >CUNKNOWN></u>
                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/866,735
FILING DATE: CUNKNOWN:
ATTORNEY/AGENT INFORMATION:
NAME: Warren, William L.
REGISTATION NUMBER: 35,714
REFERENCE/DOCKET NUMBER: 05940-0129
TELECOMMUNICATION INFORMATION:
TELEFAX: (404) 818-3700
TELEFAX: (404) 818-3799
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLONE: Plasminogen
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
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                          MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 5
US-09-761-120-1
Sequence 1, Application US/09761120
Patent No. US/0020037847A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCE CHARACTERISTICS:
LENGTH: 812 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
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Matches 106; Conservative
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ANTI-SENSE: NO
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NAME/KEY: SITE
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                                                          LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        116 SCVACGNDIALIKLSRSAQLGDAVQLASLPPAGDILPNKTPCYITGWGRLYINGPL-PDK 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        174 LQQVVLPLVTVNQCRQ--YWGARITDAMICAGGSGASSCQGDSGGPLVC-QKGNTWVLIG 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          175 LOGARLPVVDYKHCSRWNWWGSTVKKTMVCAGGYIRSGCNGDSGGPLNCPTEDGGWQVHG 234
LIKLASPARYTAQVSPVCLASTNEALPSGLTCVTTGWGRISGVGNVTPARLQQVVLPLVT 183
                                  670 LLKLSRPATITDKVIPACLPSPNYMVADRTICYITGWGETQGTFGA--GRLKEAQLPVIE 727
                                                                          184 VNQCR--QYWGARITDAMICAG--GSGASSCQGDSGGPLVCQKGNTWVLIGIVSWGTKNC 239
                                                                                                116 NTM--NNDLTLLKLASPARYTAQVSPVCLASTNEALPSGLTCVTTGWGRISGVGNVTPAR 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34.2%; Score 484.5; DB 10; Length 270; 40.9%; Pred. No. 9.2e-36; Live 43; Mismatches 100; Indels 19;
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TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies FILE REFERENCE: PAIO.
CURRENT APPLICATION NUMBER: US/09/925,297
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION UNMERS: PCT/US00/05989
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
                                                                                                                                                                                                                                                                US-09-923-779-152

Sequence 152, Application US/09923779

Patent No. US20020075721A1

GENERAL INFORMATION:
APPLICANT: Pyle, Ruth A.
APPLICANT: Ralos, Michael D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: COMPOSITIONS OF PANCREATIC CAN
FILE REPERENCE: 210121.553
CURRENT APPLICATION NUMBER: US/09/923,779

CURRENT FILIC DATE: 2001-08-06

NUMBER OF SEQ ID NOS: 155

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        235 VTSFVSGFGCNFIWKPTVFTRVSAFIDWIEETIA 268
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Patent No. US20020081659A1
GENERAL INFORMATION:
                                                                                                                                                      240 NIQAPAMYTRVSKFSTWINQVMAYN 264
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Matches 112; Conser
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LENGTH: 270
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                                                                                                                                                                                                                                                                                                                                                                                               ; LOCATION: (34)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-925-297-695
                                                                                                                                                                                                                                                                Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58 HFCGGSLISPNWVVTAAHCQVTPGRHFVVLGEYDRSSNAEPVQVLSI--ARAITHPNWNA 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NTM--NNDLTLLKLASPARYTAQVSPVCLASTNEALPSGLTCVTTGWGRISGVGNVTPAR 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LQQVVLPLVTVNQCRQ--YWGARITDAMICAGGSGASSCQGDSGGPLVC-QKGNTWVLIG 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LQQARLPVVDYKHCSRWNWWGSTVKKTMVCAGGYIRSGCNGDSGGPLNCPTEDGGWQVHG 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 MLRLLSSLILVAVASGYG-----PPSSXXSSRVVXGEDAVPYSWPWQVSLQYEKSGSFY
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| Patent No. US20020159992A1
| GENERAL INFORMATION:
| APPLICANT: Abbott Laboratories
| APPLICANT: Abott Laboratories
| APPLICANT: Davidson, Donald J.
| TITLE OF INVENTION: ANTIANGIOGENIC POLYPEPTIDES AND METHODS
| TITLE OF INVENTION: FOR INHIBITING ANGIOGENESIS
| FILE REFERENCE: 6738.US.02
| CURRENT FILING DATE: 2001-09-26
| PRIOR APPLICATION NUMBER: US 60/236,550
| PRIOR FILING DATE: 2000-09-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42; Mismatches 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34.2%; Score 484.5; DB 1
40.9%; Pred. No. 9.3e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            231 IVSWGTK-NCN-IQAPAMYTRVSKFSTWINQVMA 262
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VTSFVSGFGCNFIWKPTVFTRVSAFIDWIEETIA 271
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 791
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 928
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 695
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Best Local Similarity 40.9
Matches 112; Conservative
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                                                                                                                                                                                                                                  LOCATION: (27)
OTHER INFORMATION: X
NAME/KEY: SITE
LOCATION: (28)
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Desnoyers, Luc
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APPLICANT:
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APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT: Cao, Yihai
TITLE OF INVENTION: Materials and methods relating to endothelial cell growth
TITLE OF INVENTION: inhibitors
FILE REFERENCE: Mewburn
CURRENT APPLICATION NUMBER: 02/09/946,893
CURRENT FILING DATE: 2001-09-05
PRIOR APPLICATION NUMBER: 05 60/230,893
PRIOR FILING DATE: 2000-09-05
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.1
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                                                                                                                             | :| | || || : | :| || || 657 VITDKVIPACLPSPNYVVADRTECFITGWGETQGTFGA--GLLKEAQLPVIENKYCNRYE 714
                                                                                                                                                                          191 -WGARITDAMICAG--GSGASSCQGDSGGPLVCQKGNTWVLIGIVSWGTKNCNIQAPAMY 247
                                                                                                                                                                                                RYTAQVSPVCLASTNEALPSGLTCVTTGWGRISGVGNVTPARLQQVVLPLVTVNQCRQY- 190
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                                 76 C---QVTPGRHFVVLGEYDRSSNAEP-VQVLSIARAITHPNWNANTMNNDLTLLKLASPA 131
                                                                    CLEKSPRPSSYKVILGAH-QEVNLEPHVQEIEVSRLFLEPT-----RKDIALLKLSSPA 656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C----QVTPGRHFVVLGEYDRSSNAEP-VQVLSIARAITHPNWNANTMNNDLTLLKLASPA 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   191 -WGARITDAMICAG--GSGASSCQGDSGGPLVCQKGNTWVLIGIVSWGTKNCNIQAPAMY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 810;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 69, Application US/09978295A Patent No. US20020156006Al GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/09946893
Patent No. US20020072494A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRVSKFSTWINQVMAYN 264
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Botstein, David
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APPLICANT: Baker Kevin P.
APPLICANT: Botstein, Davi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
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LENGTH: 810
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R FILING DATE: 1998-05-15

R APPLICATION NUMBER: 60/08579

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R APPLICATION NUMBER: 60/085580

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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE OF INVENTION: Acids Encoding the Same CURRENT APPLICATION NUMBER: US/09/978,697

CURRENT APPLICATION NUMBER: US/09/9865

PRIOR APPLICATION NUMBER: 09/918685

PRIOR FILING DATE: 2001-10-16

PRIOR FILING DATE: 1997-11-03

PRIOR FILING DATE: 1997-11-03

PRIOR FILING DATE: 1997-11-13

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Goddard, Audrey
Goddwaki, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
Kuo, Sophia S.
Napier, Mary A.
Pan, James;
Paoni, Nicholas F.
Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
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DR APPLICATION NUMBER: 60/078866

DR FILING DATE: 1998-03-20

DR FILING DATE: 1998-03-20

DR APPLICATION NUMBER: 60/078916

DR FILING DATE: 1998-03-20

DR APPLICATION NUMBER: 60/078919

DR FILING DATE: 1998-03-20

DR APPLICATION NUMBER: 60/078939

DR FILING DATE: 1998-03-20

DR APPLICATION NUMBER: 60/079294

DR APPLICATION NUMBER: 60/079265

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FILING DATE: 1998-03-27
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FILING DATE: 1998-03-12
APPLICATION NUMBER: 60/078004
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Williams, P. Mickey
Wood, William I.
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Ferrara, Napoleon
Filvaroff, Ellen
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Gerber, Hanspeter
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                                                  APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
                                                                                                                                                                                                                                                        Fong, Sherman
  US20020169284A1
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### ArPLICANT: Wood, William 1.

### TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
### TITLE OF INVENTION: Acids Encoding the Same
### FILE REFERENCE: P2630PLC9
### CURRENT APPLICATION NUMBER: US/09/978,192A
### CURRENT PILING DATE: 2001-10-15
### PRIOR FILING DATE: 2001-07-30
### PRIOR FILING DATE: 1997-10-17
### PRIOR FILING DATE: 1997-11-03
### PRIOR FILING DATE: 1997-11-03
### PRIOR FILING DATE: 1997-11-03
### PRIOR FILING DATE: 1997-11-13
### PRIOR FILING DATE: 1997-11-21
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Gurney, Austin L.
Hillan, Kenneth J
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PRIOR FILING DATE: 1998-03-20
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PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078939
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APPLICATION NUMBER: 60/079294
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APPLICATION NUMBER: 60/079656
FILING DATE: 1998-03-26
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Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
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Filvaroff, Ellen
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Kuo, Sophia S.
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Eaton, Dan
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Tumas, Daniel
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APPLICANT: Ashkenaz
                                           RESULT 13
US-09-978-192A-69
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38.1%; Pred. No. 4.5e
iive 40; Mismatches
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R APPLICATION NUMBER: 60/084640

R PELLING DATE: 1998-05-07

R APPLICATION NUMBER: 60/084598

R FILING DATE: 1998-05-07

R APPLICATION NUMBER: 60/084600

R APPLICATION NUMBER: 60/084601

R APPLICATION NUMBER: 60/084601

R APPLICATION NUMBER: 60/084607

R APPLICATION NUMBER: 60/084607

R FILING DATE: 1998-5-07
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APPLICATION NUMBER: 60/083559
FILING DATE: 1998-04-29
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FILING DATE: 1998-04-29
                   FILING DATE: 1998-04-29
APPLICATION NUMBER: 60/083554
FILING DATE: 1998-04-29
APPLICATION NUMBER: 60/083558
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FILING DATE: 1998-04-30
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PRIOR PILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081838
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/082568
PRIOR PILING DATE: 1998-04-21
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R APPLICATION NUMBER: 60/080334
R PILING DATE: 1998-04-01
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R PILING DATE: 1998-04-08
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R APPLICATION NUMBER: 60/08104
R RILING DATE: 1998-04-08
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R APPLICATION NUMBER: 60/08195
R APPLICATION NUMBER: 60/081203
R FILING DATE: 1998-04-09
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R APPLICATION NUMBER: 60/079923
R FILING DATE: 1998-03-30
R APPLICATION NUMBER: 60/080105
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R APPLICATION NUMBER: 60/080165
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R FILING DATE: 1998-03-31
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FILING DATE: 1998-03-27
APPLICATION NUMBER: 60/079728
FILING DATE: 1998-03-27
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FILING DATE: 1998-04-01
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30 YNQRIVNGENAVPGSWPWQVSLQDNTGFHFCGGSLISPNWVVTAAHC---QVTPGRHFVV 86 Length 453; Indels DB 9; .5e-34; Query Match 33.0%; Score 468.5; Best Local Similarity 38.1%; Pred. No. 4.5e Matches 91; Conservative 40; Mismatches PRIOR APPLICATION NUMBER: 60/083496
PRIOR FILING DATE: 1998-04-29
PRIOR PELING DATE: 1998-04-39
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FILING DATE: 1998-05-22
APPLICATION NUMBER: 60/087098
FILING DATE: 1998-05-28
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SERRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430RLC1
CURRENT APPLICATION UNMER: US/10/052,586
CURRENT FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 60/059263
 330 ENFPDGKVCWTSGWGATEDGGDASPV-LNHAAVPLISNKICNHRDVYGGIISPSMLCAGY 388
                          R FILING DATE: 1997-09-18
R APPLICATION NUMBER: 60/059266
R FILING DATE: 1997-09-18
R APPLICATION NUMBER: 60/062250
R RFILING DATE: 1997-10-17
R APPLICATION NUMBER: 60/063120
R FILING DATE: 1997-10-24
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RR FILING DATE: 1997-10-24
RR APPLICATION NUMBER: 60/063486
R FILING DATE: 1997-10-21
R FILING DATE: 1997-10-28
R FILING DATE: 1997-10-28
R APPLICATION NUMBER: 60/063540
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FILING DATE: 1997-11-24
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FILING DATE: 1998-03-10
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FILING DATE: 1997-10-28
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                                                                                                                                                                                                                                                               Smith, Victoria
Watanabe, Colin K.
Wood, William I.
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Goddard, Audrey
Godowski, Paul J
                                                                                                                                                                                                                                     Gurney, Austin L
                                                                                                                                                                 APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
                                                                                                                                                                                                                                                     Pan, James
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Nucleic Acids, Proteins and Antibodies

Sequence 1017, Application US/09925301 Patent No. US20020052308A1

US-09-925-301-1017

RESULT 15

GENERAL INFORMATION

APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins
FILE REFERENCE: PA106
CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12

Patentin Ver. 2.0

NUMBER OF SEQ ID NOS: 1694 SOFTWARE: Patentin Ver. 2.

SEQ ID NO 1017 LENGTH: 248

; ORGANISM: Homo sapiens US-09-925-301-1017

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33.0%; Score 468.5; DB 1
ilarity 38.1%; Pred. No. 4.5e-34;
Conservative 40; Mismatches 97
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FILING DATE: 1998-06-03
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FILING DATE: 1998-06-04
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FILING DATE: 1998-06-12
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APPLICATION NUMBER: 60/087208
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                                                                  ILING DATE: 1998-06-02
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87 LGEYDRSSNAEPVQVLSIARAITHPNWNANTMNNDLTLLKLASPARYTAQVSPVCLASTN 146
                                                                                                                                                             147 EALPSGLTCVTTGWGRI-SGVGNVTPARLQQVVLPLVTVNQC--RQYWGARITDAMICAG 203
                                                                                                                                                                                                                              --GSGASSCQGDSGGPLVCQKGNTWVLIGIVSWGTKNCNIQAPAMYTRVSKFSTWINQVM 261
                                                                                                                                                                                                                                                                                                Gaps
                                                                                           30 YNQRIVNGENAVPGSWPWQVSLQDNTGFHFCGGSLISPNWVVTAAHC---QVTPGRHFVV
                                  Indels 12;
Query Match 33.0%; Score 468; DB 10; Best Local Similarity 38.3%; Pred. No. 2.4e-34; Matches 92; Conservative 40; Mismatches 96;
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Length 248;

Search completed: December 20, 2002, 15:21:07 Job time : 9.34783 secs

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DB 12; Length 453; 97; Indels

Local Similarity nes 91; Conserv

Best Loca Matches

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30 YNORIVNGENAVPGSWPWQVSLQDNTGFHFCGGSLISPNWVVTAAHC---QVTPGRHFVV 86

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1 MLLLSLTLSLVLLGSSWGCG........AMYTRVSKFSTWINQVMAYN 264
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2: /cgn2_6/ptodata/1/laa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/laa/6A_COMB.pep:*
5: /cgn2_6/ptodata/1/laa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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US-08-478-859-10
US-08-47-173-10
US-08-487-167-10
US-08-618-10-10
US-08-611-99-10
US-09-074-660-10
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US-09-106-467-10
US-08-750-711-1
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US-08-429-743-1
                                                                                                                                                                                                                                                                                                                                                            262574 seqs, 29422922 residues
                                                                                                                       December 20, 2002, 15:14:53
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Maximum DB seq length: 200000000
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Match 1
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08-09-027-337-6
Sequence 6, Application US/09027337B
Sequence 6, Application US/09027337B
Sequence 6, Application US/09027337B
Sequence 6, Application US/09027337B
Sequence 6, Application US/09027337B
PERENT INTO O'Brien, Timothy J.
APPLICANT: CO'Brien, Timothy J.
TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease Overexpressed in TITLE OF INVENTION: Breast and Ovarian Carcinomas
FILE REFERENCE: D6064
CURRENT PAPLICATION NUMBER: US/09/027,337B
CURRENT PILING DATE: 1998-02-20
NUMBER OF SEQ ID NOS: 13
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                         Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 54, Appl
Sequence 54, Appl
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 2, Appli
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    Sequence Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53.3%; Score 755.5; DB 2; Length 231; 58.2%; Pred. No. 5.7e-64; ive 35; Mismatches 61; Indels 1
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US-08-866-735-1
US-09-066-028-1
US-08-643-219-1
US-08-643-219-1
US-08-851-350-1
5200340-6
US-08-469-486-54
US-08-469-658-54
US-08-131-995-1
US-09-131-995-1
US-09-132-154-1
US-08-132-154-1
US-08-132-154-1
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US-08-132-154-1
US-08-131-1995-1
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US-08-568-031-2
US-08-966-319-2
US-09-153-304-2
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Matches 135; Conservative
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US-09-027-337-6
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LENGTH: 231
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                                                                    Query Match
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Sequence 6, Application US,09644600 Patent No. 6451500 GENERAL INFORMATION: APPLICANT: O'Brien, Timothy J. APPLICANT: Tanimoto, Hirotoshi

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(212) 354-8113
  APPLICATION NUMBER:
                      FILING DATE:
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US-08-557-146-13
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APPLICANT: GRANADOS, EDWARD N.
APPLICANT: KLASS, MICHAEL R.
APPLICANT: KLASS, MICHAEL R.
APPLICANT: STEWART, KENT D.
APPLICANT: STRONDE, STEVEN D.
APPLICANT: STRONDE, STEVEN D.
APPLICANT: TILLE OF INVENTION: AND METHODOS USEFUL FOR DETECTING AND TREATING DISEASES TITLE OF INVENTION: OF THE PROSTATE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93 SSNAEPVQVLSIARAITHPNWNANTMNNDLTLLKLASPARYTAQVSPVCLASTNEALPSG 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                153 LTCVTTGWGRISGVGNVTPARLQQVVLPLVTVNQCRQYWGARITDAMICAGGSGASSCQG 212
                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease
                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                             Query Match 53.3%; Score 755.5; DB 4; Best Local Similarity 58.2%; Pred. No. 5.7e-64; Matches 135; Conservative 35; Mismatches 61;
                Overexpressed in Carcinomas
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SOFTWARE: FastESO for Windows Version 2.0
CAPPLICATION DATA:
APPLICATION NUMBER: US/08/944,483
                                FILE REFERENCE: D6064CIP/D
CURRENT APPLICATION UNDABER: US/09/644,600
CURRENT FILING DATE: 1000-08-23
PRIOR APPLICATION NUMBER: 09/421,213
PRIOR FILING DATE: 1999-10-20
PRIOR FILING DATE: 1999-02-20
NUMBER OF SEQ ID NOS: 98
SEQ ID NO 6
SEQ ID NOS: 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 62, Application US/08944483; Patent No. 6232456; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3: Abbott Laboratories
100 Abbott Park Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COLPITTS, TRACEY L. FRIEDMAN, PAULA N. GRANADOS, EDWARD N.
                                                                                                                                                                                                                                                                 FEATURE:
; OTHER INFORMATION: Chymotrypsin
US-09-644-600-6
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COMPUTER READABLE FORM:
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PRIOR APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott La
STREET: 100 Abbott P
                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM:
                  TITLE OF INVENTION:
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154 TCVTTGWGRISGVGNVTPARLQQVVLPLVTVNQCRQYWGARITDAMICAGGSGASSCQGD 213
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Patent No. 5834290
GENERAL INFORMATION:
APPLICANT: Egglrud, Torbjorn
APPLICANT: Hansson, Lennart
TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
TITLE OF INVENTION: Enzyme (SCCE)
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: White & Case, Patent Department
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   180 SGGPLVCQKDGAWTLVGIVSWGSDTCSTSSPGVYARVTKLIPWVQKILAAN 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     214 SGGPLVCQKGNTWVLIGIVSWGTKNCNIQAPAMYTRVSKFSTWINQVMAYN 264
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/557,146
FILING DATE: U1-DEC-1995
CLASSIFICATION: 4.24
                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 52.9%; Score 750.5; DB 4
Best Local Similarity 58.0%; Pred. No. 1.7e-63;
Matches 134; Conservative 35; Mismatches 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: White & Case, Patent Department STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Sterner, Richard J.
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-181
TELECOMMUNICATION INFORMATION:
                                                                                6183.US.01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2787
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                           NAME: Becker, Cheryl L. REGISTRATION NUMBER: 35,441
                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear
; MOLECULE TYPE: No. 6232456e
US-08-944-483-62
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CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 230 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                       TELEX:
INFORMATION FOR SEQ ID NO:
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94 SNAEPVQVLSIARAITHPNWNANTMNNDLTLLKLASPARYTAQVSPVCLASTNEALPSGL 153
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                                                                                                                                                            1 IVNGEDAVPGSWPWQVSLQDKTGFHFCGGSLISEDWVVTAAHCGVRTS-DVVVAGEFDQG 59
                                                                                                                                      34 IVNGENAVPGSWPWQVSLQDNTGFHFCGGSLISPNWVVTAAHCQVTPGRHFVVLGEYDRS 93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Analog of Haemophilus Hin47 Protein with TITLE OF INVENTION: Reduced Protease Activity NUMBER OF SEQUENCES: 23 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 228;
                                                                                                                                                                                                                                                                                                                                                                              214 SGGPLVCQKGNTWVLIGIVSWGTKNCNIQAPAMYTRVSKFSTWINQVMAYN 264
                                                                                                                                                                                                                                                                                                                                                                                                     Length 229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Toronto
STATE: Ontario
COMPREN: Canada
21P: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PIBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/278,091
FILING DATE: 21-JUL-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 724.5; DB 1
Pred. No. 4.9e-61;
                                                           Score 737; DB 2;
Pred. No. 3.2e-62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51.1%; Sco. 57.1%; Pred. No. 4... 57.1%; Mismatches
                                                                                               36; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Sim & McBurney
Suite 701, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 10, Application US/08278091
Patent No. 5506139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: LOOSMORE, Sheena M
APPLICANT: YANG, Yan-Ping
APPLICANT: CHONG, Pele
APPLICANT: CHOME, Raymond P.
APPLICANT: KLEIN, Michel H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                           52.0%;
57.6%;
  polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 228 amino acids
amino acid
                                                                                                 Conservative
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linear
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Best Local Similarity
                                                           Ouery Match
Best Local Similarity
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  MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 6
US-08-278-091-10
          ; MULECULE 111
US-09-154-344-13
                                                                                                 Matches 133;
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                                                                                                                                                                                                                                                                            34 IVNGENAVPGSWPWQVSLQDNTGFHFCGGSLISPNWVVTAAHCQVTPGRHFVVLGEYDRS 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Egalrud, Torbjorn
APPLICANT: Hansson, Lennart
TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
TITLE OF INVENTION: Enzyme (SCCE)
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: White & Case, Patent Department
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   214 SGGPLVCQKGNTWVLIGIVSWGTKNCNIQAPAMYTRVSKFSTWINQVMAYN 264
                                                                                                                                                                             Length 229;
                                                                                                                                                                         52.0%; Score 737; DB 2; Length 22
57.6%; Pred. No. 3.2e-62;
tive 36; Mismatches 60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
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Patent No. 5981256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (212) 819-8783
TELEPAX: (212) 34-8113
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 229 amino acids
TYPE: amino acids
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Sterner, Richard J.
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 111
TELECOMMUNICATION INFORMATION:
INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06
FILING DATE: 14-DEC-1995
CLASSIFICATION:
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                                                                                           ; TOPOLOGY: linear
; MOLECULE TYPE: polypeptide
US-08-557-146-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-SEP-1998
                                  LENGTH: 229 amino acids
TYPE: amino acids
STRANDEDNESS: single
                                                                                                                                                                                                               Conservative
                    SEQUENCE CHARACTERISTICS
                                                                                                                                                                             Query Match
Best Local Similarity
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STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                 Matches 133;
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
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                                                                                                                                                                                                                                                                     RESULT 8
US-08-472-173-10
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                                                                               60 SSSEKIQKLKIAKVFKNSKYNSLTINNDITLLKLSTAASFSQTVSAVCLPSASDFAAGT 119
                                                                                                                                154 TCVTTGWGRISGVGNVTPARLQQVVLPLVTVNQCRQYWGARITDAMICAGGSGASSCQGD 213
                                                                                                                                                        94 SNAEPVQVLSIARAITHPNWNANTMNNDLTLLKLASPARYTAQVSPVCLASTNEALPSGL 153
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1 IVNGEBAVPGSWPWQVSLQDKTGFHFCGGSLINENWVVTAAHCGVTTS-DVVVAGEFDQG 59
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                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: LOGSWORE, Sheena M.
APPLICANT: YANG, Yan-Ping
APPLICANT: CHONG, Pele
APPLICANT: CHONG, Pele
APPLICANT: COMEN, Raymond P.
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: Ranladgo of Haemophilus Hin47 Protein with
TITLE OF INVENTION: Reduced Protease Activity
                                                                                                                                                                                                                               178 SGGPLVCKKNGAWILVGIVSWGSSICSISIPGVYARVIALVNWVQQILAAN 228
                                                                                                                                                                                                           214 SGGPLVCQKGNTWVLIGIVSWGTKNCNIQAPAMYTRVSKFSTWINQVMAYN 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 724.5; DB 1
; Pred. No. 4.9e-61;
34; Mismatches 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Sim & McBurney
Suite 701, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 1038-495 MIS:vg TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 07-UN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/296,149
FILING DATE: 26-AUG-1994
PRIOR APPLICATION NUMBER: US 08/278,091
FILING DATE: 21-JUL-1994
ATTORNEY AGENT INFORMATION:
NAME: Stewart, Michael I.
REGISTRATION NUMBER: 24,933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/483,859
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                          Sequence 10, Application US/08483859
Patent No. 5656436
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (416) 595-1155
TELERAX: (416) 595-1163
INPORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 228 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51.1%;
57.1%;
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COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBui
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
TOPOLOGY: linear
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Best Local Similarity
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US-08-483-859-10
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94 SNAEPVQVLSIARAITHPNWNANTMNNDLTLLKLASPARYTAQVSPVCLASTNEALPSGL 153
SNAEPVQVLSIARAITHPNWNANTMNNDLTLLKLASPARYTAQVSPVCLASTNEALPSGL 153
                                                                                                                            1 IVNGEEAVPGSWPWQVSLQDKTGFHFCGGSLINENWVVTAAHCGVTTS-DVVVAGEFDQG 59
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                                                                                                  TCVTTGWGRISGVGNVTPARLQQVVLPLVTVNQCRQYWGARITDAMICAGGSGASSCQGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of Haemophilus Hin47 Protein with
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                                                                                                                                                                                                                         SGGPLVCQKGNTWVLIGIVSWGTKNCNIQAPAMYTRVSKFSTWINQVMAYN 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,173
FILING DATE: US-JUN-1995
CLASSIFICATION: 435
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Reduced Protease Activity
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Suite 701, 330 University Avenue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/296,149
FILING DATE: 26-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/278,091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 08/278,091
FILING DATE: 21-JUL-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                       Sequence 10, Application US/08472173 Patent No. 5665353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: Canada
ZIP: MAGG IRA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: ISM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-D
SOFTWARE: Patentin Release #1
                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: LOOSMORE, Sheena M
APPLICANT: YANG, Yan-Ping
APPLICANT: CHONG, Pele
CHONG, Pele
APPLICANT: COMEN, RAYMOND P.
APPLICANT: KLEIN, Michel H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Stewart, Michael I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 10.
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 10:
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CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
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ADDRESSEE:
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US-08-482-816-10
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213
                                                                  SNAEPVQVLSIARAITHPNWNANTMNNDLTLLKLASPARYTAQVSPVCLASTNEALPSGL 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of Haemophilus Hin47 Protein with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 228;
                                                                                                                                SGGPLVCQKGNTWVLIGIVSWGTKNCNIQAPAMYTRVSKFSTWINQVMAYN 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,167
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                      APPLICANT: LOOSMORE, Sheena M.
APPLICANT: LOOSMORE, Sheena M.
APPLICANT: TANG, Yan-Ping
APPLICANT: CHONG, Pele
APPLICANT: CHONG, Pele
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: Analog of Haemophilus Hin47
TITLE OF INVENTION: Reduced Protease Activity
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 51.1%; Score 724.5; DB 2; Best Local Similarity 57.1%; Pred. No. 4.9e-61; Matches 132; Conservative 34; Mismatches 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE DOCKET NUMBER: 1338-508 MIS:vg
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROOF APPLICATION 173.

PROOF APPLICATION DATA:
APPLICATION NUMBER: US 08/296,149
FILING DATE: 26-ADG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/278,091
FILING DATE: 21-JUL-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                            Sequence 10, Application US/08487167
Patent No. 5869302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Stewart, Michael I. REGISTRATION NUMBER: 24,973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 228 amino acids
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M5G 1R7
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CITY: Toronto
STATE: Ontario
COUNTRY: Canada
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GENERAL INFORMATION:
APPLICANT: LOOSMORE, Sheena M
APPLICANT: TANG, Yan-Ping
APPLICANT: GOMEN, Raymond P
APPLICANT: CHONG, Pele
APPLICANT: KLEIN, Michel H
TITLE OF INVENTION: Analog of Haemophilus Hin47 Protein with Reduced Protease //
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'n
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                                                94 SNAEPVQVESIARAITHPNWNANTMNNDLTLLKLASPARYTAQVSPVCLASTNEALPSGL 153
TCVTTGWGRISGVGNVTPARLQQVVLPLVTVNQCRQYWGARITDAMICAGGSGASSCQGD 213
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SOFTWARE PATENTING STATES.

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/482,816

FILING DATE: US/08/482,816

FILING DATE: US/08/482,816

PRIOR APPLICATION DATA:

APPLICATION DATA:

PRILICATION DATE: 26-AUG-1994

PRIOR APPLICATION DATA:

FILING DATE: 21-JUL-1994

ATTORNEY/AGENT INFORMATION:

NAME: STEWART, MICHAEL INFORMATION:

NAME: STEWART, MICHAEL INFORMATION:

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NAME: STEWART, 
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Pred. No. 4.9e-61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51.1%; Sco...
57.1%; Pred. No. 4...
'''a 34; Mismatches
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Suite 701, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 10, Application US/08482816 Patent No. 5935573
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 228 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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FILING DATE:
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US-08-801-499-10
   US-08-801-499-10
                                                                         APPLICANT:
APPLICANT:
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120 TCVTTGWG-LTRYAN-TPDRLQQASLPLLSNTNCKKYWGTKIKDAMICAGASGVSSCMGD 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              154 TCVTTGWGRISGVGNVTPARLQQVVLPLVTVNQCRQYWGARITDAMICAGGSGASSCQGD 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34 IVNGENAVPGSWPWQVSLQDNTGFHFCGGSLISPNWVVTAAHCQVTPGRHFVVLGEYDRS 93
                                                                                                                      Length 228;
                              SGGPLVCQKGNTWVLIGIVSWGTKNCNIQAPAMYTRVSKFSTWINQVMAYN 264
                                            SGGPLVCQKGNTWVLIGIVSWGTKNCNIQAPAMYTRVSKFSTWINQVMAYN 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51.1%; Score 724.5; DB 2; illarity 57.1%; Pred. No. 4.9e-61; Conservative 34; Mismatches 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-390
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFRX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 228 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/296,149
                                                                                                                                                                                                                                                                                                                                                                          COMUNIA.
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
AudityER: IBM PC compatible
COMPATIBLE PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 132; Conserva
                                                                                                                                                                                                                                                                                                                                                                        Canada
                                                                                                                                                                                                                                                                                                                ADDALL
STREET: Sur.
TTTY: Toronto
                                                                                                                                                                                                                                                                                                                                                            Ontario
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE
                                                                                                                   US-08-296-149-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-296-149-10
                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                              214
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                                                                                                      RESULT 11
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APPLICANT: CHONG, Pele
APPLICANT: OOMEN, Raymond P.
APPLICANT: KIEIN, Michel H.
TITLE OF INVEXTION: Analog of Haemophilus Hin47 Protein with Reduced Protease A
NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             154 TCVTTGWGRISGVGNVTPARLQQVVLPLVTVNQCRQYWGARITDAMICAGGSGASSCQGD 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 IVNGEEAVPGSWPWQVSLQDKTGFHFCGGSLINENWVVTAAHCGVTTS-DVVVAGEPDGG 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34 IVNGENAVPGSWPWQVSLQDNTGFHFCGGSLISPNWVVTAAHCQVTPGRHFVVLGEYDRS 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/801,499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51.1%; Score 724.5; DB 2 57.1%; Pred. No. 4.9e-61;
                                                                                                                                                                                                                                                                    ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
CITY: Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-671 MIS:jb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/482,816
FILING DATE: 07-UN-1995
PRIOR APPLICATION NUMBER: US 08/296,149
FILING DATE: 26-AUG-1994
PRIOR APPLICATION NUMBER: US 08/278,091
FILING DATE: 21-UL-1994
APPLICATION NUMBER: US 08/278,091
FILING DATE: 21-UL-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
Sequence 10, Application US/08801499
Patent No. 5962430
GENERAL INFORMATION:
APPLICANT: LOCSMORE, Sheena M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 10
                                                                                                   YANG, Yan-Ping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                       STATE: Ontario
COUNTRY: Canada
ZIP: MSG 1R7.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match_
Best Local Similarity
Matches 132; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
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RESULT 12

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60 SSSEKIQKLKIAKVFKNSKYNSLTINNDITLLKLSTAASFSQTVSAVCLPSASDFAAGT 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34 IVNGENAVPGSWPWQVSLQDNTGFHFCGGSLISPNWVVTAAHCQVTPGRHFVVLGEYDRS 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCVTTGWGRISGVGNVTPARLQQVVLPLVTVNQCRQYWGARITDAMICAGGSGASSCQGD
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: Analog of Haemophilus Hin47 Protein with
TITLE OF INVENTION: Reduced Protease Activity
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 3; Length 228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  214 SGGPLVCQKGNTWVLIGIVSWGTKNCNIQAPAMYTRVSKFSTWINQVMAYN 264
                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/074,660
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4.9e-61;
                                                                                      ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1038-731 MIS: Jb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51.1%; Score 724.5;
57.1%; Pred. No. 4.9¢
tive 34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/487,167
FILING DATE: 07-0704-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/296,149
FILING DATE: 26-MG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/278,091
FILING DATE: 21-0704-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 10, Application US/09074659
Patent No. 6025342
GENERAL INFORMATION:
APPLICANT: LOOSMORE, Sheena M.
APPLICANT: YANG, Yan-Ping
APPLICANT: CHONG, Pele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 228 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24,973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Stewart, Michael I
REGISTRAILION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1
TELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: single
                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 132; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                          COUNTRY: Canada
ZIP: M5G 1R7
                                                                                                                                                                       STATE: Ontario
COUNTRY: Canada
                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-074-659-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-074-660-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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              Sequence 10, Application US/08615271

Patent No. 5981503

GENERAL INFORMATION:
APPLICANT: LOOSMORE, Sheena M.
APPLICANT: TANG, Yan-Ping
APPLICANT: OMEN, Raymond P.
APPLICANT: CHONG, Pele
APPLICANT: COMEN, Raymond P.
TITLE OF INVENTION: PROTEASE ACTIVITY
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS: 23
CORRESPONDENCE ADDRESS: 330 University Avenue
CITY: Toronto
STREET: Gth Floor, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SGGPLVCQKGNTWVLIGIVSWGTKNCNIQAPAMYTRVSKFSTWINQVMAYN 264
                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 20-JUN-1996
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51.1%; Score 724.5; DB 57.1%; Pred. No. 4.9e-61
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Patent No. 6020183
GENERAL INFORMATION:
APPLICANT: LOSMORE, Sheena M.
APPLICANT: YANG, Yan-Ping
APPLICANT: CHONG, Pele
APPLICANT: OOMEN, Raymond P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1163
INFORMATION FOR SEQ ID NO: 10:
SEQUIENCE CHARACTERISTICS:
LENGTH: 228 anino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 57.18
Matches 132; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single
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US-09-074-660-10
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        US-08-615-271-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3;
                                   TITLE OF INVENTION: Analog of Haemophilus Hin47 Protein with TITLE OF INVENTION: Reduced Protease Activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 3; Length 228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   214 SGGPLVCQKGNTWVLIGIVSWGTKNCNIQAPAMYTRVSKFSTWINQVMAYN 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                       CITY: Toronto
STATE: Ontario
COMPUTER: Canada
ZIP: MSG IR/
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/074,659
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51.1%; Score 724.5; DB 3.
57.1%; Pred. No. 4.9e-61;
tive 34; Mismatches 62.
                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/487,167
FILING DATE: 07-UN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/296,149
FILING DATE: 26-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/278,091
FILING DATE: 21-UL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I.
REGISTATION NUMBER: 24,973
REGISTATION NUMBER: 24,973
REGISTATION NUMBER: 24,973
REGISTATION NUMBER: 24,973
REGISTATION NUMBER: 24,973
REGISTATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-730 MIS:jb
                                                                           NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSES: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
CITY: Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 228 amino acids
TYPE: amino acid
STRANDEDNESS: single
OOMEN, Raymond P. KLEIN, Michel H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 57.19
Matches 132; Conservative
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US-09-074-659-10
  APPLICANT:
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Search completed: December 20, 2002, 15:20:37 Job time : 15.9565 secs

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091674 xenopus lae 091674 xenopus lae 094760 paraalichthy 091039 gadus morhu 091846 homo sapien 096679 homo sapien 096679 homo sapien 096679 acclopendra 019023 macaca mula 019023 macropus eu 092044 mus musculu 0950483 macropus eu 08976 mus musculu 09506 petromyzon 04268 petromyzon 04268 petromyzon 04158 mus musculu 08676 mus musculu 08676 mus musculu 08618 mus musculu 08189 mus musculu 08189 mus musculu 08189 mus musculu 08189 mus musculu 08189 mus musculu 08189 mus musculu 08189 mus musculu 08189 mus musculu 089408 mus musculu 08189 mus musculu 089408 mus musculu 089408 mus musculu 089408 mus musculu 089408 mus musculu 089408 mus musculu 089408 mus musculu 089408 mus musculu 089408 musuutus norv

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mitsui S., Yamaguchi N.;
"Molecular cloning of mouse chymopasin.";
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
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01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
CTRL OR CTRAl.
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MGD; MGI:8858; Ctl.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
Pfan; PR00089; trypsin; 1.
SRINTS; PR00722; CHYMOTRYPSIN.
SRART; SM00020; Tryp_SPC; 1.
PROSITE; PS00134; TRYPSIN_DIS; UNKNOWN_1.
PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
Hydrolase; Serine protease.
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              Q9W7Q1
Q91674
Q9W7Q0
Q91039
Q91WJ5
Q15146
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0921R9
Q8R1A6
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Q8QGW3
Q920K3
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STRAIN-129S6/SVEVTAC; TISSUE-SPLEEN;
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O18783
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Q8VDE0
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091X79
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Q99L44
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                                                                                                                  PRELIMINARY;
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 NCBI_TaxID=10090;
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Q9ER05
 094708 mus musculu 0964960 mus musculu 0964828 rattus norv 09w7q4 paralichthy 09w7q4 paralichthy 09w7q3 paralichthy 09c868 mus musculu 09c808 mus musculu 09c9c52 mus musculu 09c452 mus musculu 09c452 mus musculu 09c479 mus musculu 09c779 qadus morhu 09c779 qadus morhu 09w7p9 paralichthy 09bk47 luidia foli
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1663.721 Million cell updates/sec
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                                                                                                December 20, 2002, 15:14:08 ; Search time 32.6957 Seconds
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                                                                                                                                                      US-09-856-319B-4
1418
1 MLLLSLTLSLVLLGSSWGCG......AMYTRVSKFSTWINQVMAYN
              GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                     OM protein - protein search, using sw model
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09907P8
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sp_plant:*
sp_rodent:*
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sp_virus:*
sp_vertebrate:*
sp_unclassified:*
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Gapop 10.0 , Gapext 0.5
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2: sp_bacteria:*
3: sp_fung1:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
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sp_bacteriap:*
sp_archeap:*
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Maximum DB seq length: 2000000000
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533.5
510
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Perfect score:
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Database

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Sequence:

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PRINTS; PR00722; CHYMOTRYPSIN.
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RA KAWAI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Radawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Radito T., Oƙazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Radota K., Matsuda H.A., Sizuki R., Tomita M., Wagner L., Washio T.,
Rakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Rawishim M.J., Bult C., Fletcher C., Fullita M., Gariboldi M.,
Rayonstein M.J., Bult C., Fletcher C., Fullita M., Mombaerts P.,
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Rotinoich S., Hill D., Hofman M., Hume D.A., Kamiya M., Lee N.H.,
Rosaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Rymshaw-Bootis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
Rymshaw-Bootis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection.";
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                            Length 264;
                                                     Indels
 28135 MW; 1D979709A07056C2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                         Query Match 100.0%; Score 1418; DB 11; Best Local Similarity 100.0%; Pred. No. 1.4e-118; Matches 264; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                  264 AA.
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InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00089; trypsin; 1.
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                                                                                                                                                                                                                                                                                        IQAPAMYTRVSKFSTWINQVMAYN 264
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CTRL OR 1810004D15RIK.
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264 AA;
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 SEQUENCE
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
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                                                                                                                                                                                                       Length 264;
                                                                                                                                             28167 MW; 1D979469A07056C2 CRC64;
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Last annotation update)
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Pred. No. 3.1e-118;
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0; Mismatches
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UNKNOWN_1.
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STRAIN-C57BL/6J; TISSUE-PANCREAS;
MEDLINE-21085660; Pubmed-11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 IQAPAMYTRVSKFSTWINQVMCYN 264
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SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS50240; TRYPSIN_DOM;
PROSITE; PS500134; TRYPSIN_HIS;
PROSITE; PS00135; TRYPSIN_SER;
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                                                                                                                                                                                                       99.78;
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                                                                                                                  Hydrolase; Serine protease.
SEQUENCE 264 AA; 28167 M
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Best Local Similarity 99.6
Matches 263; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2001 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
1810004D15Rik protein.
CTRL OR 1810004D15RIK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRYPSIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2001
01-JUN-2001
                                                                                                                                             SEQUENCE
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Q9D960;
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Query Match
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09W7Q4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 GGSLISPNWVVTAAHCQVTPGRHFVVLGEYDRSSNAEPVQVLSIARAITHPNWNANTMNN 120
                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                   1 MLLLSLTLSLVLLGSSWGCGVPAITPALSYNQRIVNGENAVPGSWPWQVSLQDNTGFHFC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <u>ب</u>
                                                                                                                                                                                                                                                                                                                                                                       DLTLLKLASPARYTAQVSPVCLASTNEALPSGLTCVTTGWGRISGVGNVTPARLQQVVLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LVTVNQCRQYWGARITDAMICAGGSGASSCQGDSGGPLVCQKGNTWVLIGIVSWGTKNCN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
TISSUE-RAT PANCREAS;
Sogame Y., Mitsui S., Kataoka K., Kashima K., Kato M., Sakagami
Yamaquchi N.;
                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Molecular cloning of rat chymopasin.";
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS
                                                                                                                                                                                                                                                                          Length 264;
                              MDD, MGI:88658; CITI.
InterPro: IPR001314; Chymotrypsin.
InterPro: IPR001324; Set_protease_Try.
Pfam; PR00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM0020; TRYP_SRO.
II.
PROSITE; PS50240; TRYPSIN_LND, 1.
PROSITE; PS50134; TRYPSIN_LND, 1.
PROSITE; PS00134; TRYPSIN_LND, 1.
PROSITE; PS00135; TRYPSIN_LND, 1.
PHYTOLASS; Setline protease.
SEQUENCE 264 AA; 28151 MW; 1D979719E07C16DE CRC64;
                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28116 MW; F9ED5D210FD3500E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                    99.3%; Score 1408; DB 11;
99.6%; Pred. No. 1.1e-117;
11ve 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ¥.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRYPSIN FAMILY.
EMBL; AB020757; BAB20287.1; -.
HSSP; P00766; 4CHA.
                                                                                                                                                                                                                                                                                          Best Local Similarity 99.6
Matches 263; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEROPS; S01.256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chymopasin.
                                                                                                                                                                                                                                                                          Query Match
Best Local 3
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Q9EQZ8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181
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GGSLISPNWVVTAAHCQVTPGRHFVVLGEYDRSSNAEPVQVLSIARAITHPNWNANTMNN 120
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                                                                                                                                                                                                           GGSLISPNWVVTAAHCQVTPGRHFVVLGEYDRSSNAEPVQVLSIARAITHPNWNANTMNN 120
                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Paralichthys Olivaceus (Flounder).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Ectinopterygii; Neopterygii; Teleosstei; Neoteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
Pleuronectoidei; Paralichthyidae; Paralichthys.
                                                                                                                                LVTVNQCRQYWGARITDAMICAGGSGASSCQGDSGGPLVCQKGNTWVLIGIVSWGTKNCN
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                                                                                                        1 MLLLSLTLSLVLLGSSWGCGVPAITPALSYNQRIVNGENAVPGSWPWQVSLQDNTGFHFC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-PANCERS;
Suzuki T., Srivastava A.S., Kurokawa T.;
Suzuki T., Srivastava A.S., Kurokawa T.;
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI; ALSO KNOWN AS:
TRYPSIN FAMILY.
EMBL, RAB029753; BAA82365.1; -.
HSSP; P00763; 1DPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 13; Length 261;
  Length 264;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63.1%; Score 894.5; DB 13; Length
63.0%; Pred. No. 6.6e-72;
.ive 33; Mismatches 60; Indels
                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hydrolase; Serine protease.
SEQUENCE 261 AA; 28184 MW; D7090A9D65395B7D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TrEMBLrel. 12, Last sequence update) (TrEMBLrel. 21, Last annotation update)
96.3%; Score 1365; DB 11; 93.6%; Pred. No. 7.2e-114; iive 16; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; JUL 200; IPR001214; Chymotrypsin. InterPro; IPR001254; Ser_protease_Try. Pfam. PF00089; trypsin; I. SMRT; SM00020; CHYMOTRYPSIN. SMART; SM00020; Tryp_SPC; I. PROSITE; PS00210; Tryp_SPC; I. PROSITE; PS00134; TRYPSIN_BOM; I. PROSITE; PS00135; TRYPSIN_HIS; UNKNOWN_I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last seq
01-JUN-2002 (TrEMBLrel. 21, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 IQAPAMYTRVSKFSTWINQVMAYN 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 VQAPAMYTRVSKFNTWINOVIAYN 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 63.0%
Matches 167; Conservative
                                                  Matches 247; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chymotrypsinogen 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEROPS; S01.256; -
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Best Loca
Matches
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                                                              HID DAY READ DRY READ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70 VVTAAHCQVTPGRHFVVLGEYDRSSNAEPVQVLSIARAITHPNWNANTMNNDLTLLKLAS 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67 VYTAAHCNVRTS-HRVILGEHDRSSSAEDIQVMKVGKVFKHPRYNGYTINNDILLIKLAA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  130 PARYTAQVSPVCLASTNEALPSGLTCVTTGWGRISGVGNVTPARLQQVVLPLVTVNQCRQ 189
                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes; Pleuronectoidei; Paralichthyidae; Paralichthys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=PANCREAS;
Suzuki T., Srivastava A.S., Kurokawa T.;
Suzuki T., Srivastava for chymotripsinogen 2.";
Submitted (JUL-1999) to the EMBL/Genbank/DDBJ databases.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
                                                                                                       LISPAQCKQYWGYNRITDAMICAGASGVSSCQGDSGGPLVCEKSGAWFLTGIVSWGTSNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 LVLLGSSWGCGVPAITPALSYNQRIVNGENAVPGSWPWQVSLQDNTGFHFCGGSLISPNW
DLTLLKLASPARYTAQVSPVCLASTNEALPSGLTCVTTGWGRISGVGNVTPARLQQVVLP
                                                                                     LVTVNQCRQYWG-ARITDAMICAGGSGASSCQGDSGGPLVCQKGNTWVLIGIVSWGTKNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 805.5; DB 13; Lewy...
Pred. No. 5.7e-64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9F583044E22F78C0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel. 12, Last sequence update) (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                               260 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEMORS; SOL.132; ...
INTERPRO; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
Pfan; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
PROSITE; PS50240; TRYP_SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_LSE; 1.
Hydrolase; Serine protease.
SEQUENCE 260 AA; 27793 MW; 9F583044E22F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40; Mismatches
                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1999 (TrEMBLrel. 12, Created)
                                                                                                                                                                        NIQAPAMYTRVSKFSTWINQVMAYN 264
                                                                                                                                                                                                 Chymotrypsinogen 2.
Paralichthys olivaceus (Flounder).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRYPSIN FAMILY.
EMBL, AB029754; BAA82366.1; -.
HSSP; P00766; 1CHG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VTELRAWMDQTIANN 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           250 VSKFSTWINQVMAYN 264
                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
es 143; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEROPS; S01.152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=8255
                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1999
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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Matches
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                                          119
                                                                                                                                                                             240
                                                                                                                             177
                                                                                                                                                                                                                     237
                                                                                                                                                                                                                                                                                    RESULT 6
Q9W7Q3
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SUZENCE TRAINCSTEL, 63: TISSUE-SPLEEN;

A RAMAI J., Shinaqawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A RAWAI J., Shinaqawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A Arakawa T., Hara A., Ribibata K., Kiyosawa H., Rondo S., Yamanaka I.,

A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Radto T., Okazaki Y., Gojobori T., Bono H., Rasukawa T., Saito R.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radta K., Okido T., Futuno M., Anno H., Baddarelli R., Barsh G.,

Bakai K., Okido T., Futuno M., Anno H., Baddarelli R., Barsh G.,

Bakai K., Okido T., Futuno M., Anno H., Baddarelli R., Barsh G.,

Bakai K., Okido T., Futuno M., Anno H., Baddarelli M., Gariboldi M.,

Burke J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Bronstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Rordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Ry Nynshaw-Bonis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Panakai M., Kanakai S.,

Ryanakai M., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 LVTVNQCRQYWGARITDAMICAGGSGASSCQGDSGGPLVCQKGNTWVLIGIVSWGTKNCN 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGSLISPNWVVTAAHCQVTPGRHFVVLGEYDRSSNAEPVQVLSIARAITHPNWNANTMNN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DLTLLKLASPARYTAQVSPVCLASTNEALPSGLTCVTTGWGRISGVGNVTPARLQQVVLP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 GGSLISENWAVTAAAHCGVKT-TNVVVAGEFDQGSDEENVQVLKIAQVFKNPKFNSFTVRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MLLLSLTLSLVLLGSSWGCGVPAITPALSYNQRIVNGENAVPGSWPWQVSLQDNTGFHFC
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                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 409:685-690(2001).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS
TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS: PRO0722; CHYMOTRYPSIN.
PRINTS: PR00722; CHYMOTRYPSIN.
SMART; SM00020; TTYP_SPC. 1.
PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
PROSITE; PS00135; TRYPSIN_HIS; UNKNOWN_1.
Hydrolase; Serine protease;
SEQUENCE 263 AA; 27821 MW; 2620A27AFBA5D04D CRC64;
                                                               01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGD; MGI:1913723; 2200008D09Rik.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AK003060; BAB22539.1; -. HSSP; P00766; 1GCT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                             ut-JUN-2001 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
2200008D09Rik protein.
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
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RESULT 8 Q9CR35

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1 MAFLWLVSCFALVGATFGCGVPAIQPVLTGLSRIVNGEDAIPGSWPWQVSLQDRTGFHFC 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        240 TSTPAVYARVTALMPWVQEILEAN 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 IQAPAMYTRVSKFSTWINQVMAYN 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2200008D09Rik protein.
2200008D09RIK.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID-10090;
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KEANAI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Eukuda S.,

A Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Salto T., Okazaki Y., Gojobori T., Bono H., Rasukawa T., Salto R.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.P., Suzuki R., Tomita M., Wagner L., Washio T.,

A Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Rosching P., Marchional L., Mashima J., Mazaraelli J., Mondone P.,

Nordone P., Ring B., Ringwald M., Rodiguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Ruzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Masashizaki Y.,

Masashizaki Y.,

Masasaki Y., Kawaji H., Kohtsuki S.,

A Hayashizaki Y.,

Kawashizaki W.,

Kawashizaki W.,

Kawashizaki W.,

Kawashizaki W.,

Kawashizaki W.,

Kawashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ä
Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 409:685-690(2001).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 11; Length 263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56.1%; Score 795.5; DB 11; Length
54.9%; Pred. No. 4.5e-63;
Live 41; Mismatches 77; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27822 MW; 28C4487AF1A26B27 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     263 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UNKNOWN 1.
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InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001204; Ser_protease_Try
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam, PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00202; Tryp_SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; UNKNC
PROSITE; PS00135; TRYPSIN_SER; 1.
Hydrolase; Serine procease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                       241 IQAPAMYTRVSKFSTWINQVMAYN 264
                                                                                                                                                                                                                                                        240 TSTPAVYARVTALMPWVQEILEAN 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BAB25241.1; -. BAB25280.1; -. BAB25861.1; -. BAB25954.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AK008927; BAB25971.1; -. EMBL; AK003079; BAB22553.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 54.99
Matches 145; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2200008D09R1k protein.
2200008D09R1K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AK007815; BAB2
EMBL; AK008729; BAB2
EMBL; AK008888; BAB2
HSSP; P00766; IGCT
MEROPS; S01.152; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    263 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AK007765; FAK007815; FAK07815; FAK07855; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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A Rawal U., Shinagawa A., Shibata X., Yoshino M., Itoh M., Ishii Y., A Arakawa T., Hara A., Shibata X., Konno H., Adachi J., Fukuda S., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Alawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Asito T., Okazaki Y., Gojobori T., Baton H., Rasukawa T., Saito R., A Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Ashellan W., Gasaterland T., Gissi C., King B., Kochiwa H., A Lewis S., Matsuo Y., Mikaldo I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuki R., Tomita M., Wagner L., Washio T., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Rousine P., Marchionni L., Mashima M., Hume D.A., Kamiya M., Lee N. H., Saban V., Schoenbach C., Seya T., Shibata Y., Storch K.F., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.F., Wang K.H., Weitz C., Whittaker C., Wilming L., Masshizaki Y., Kawaji H., Kohtsuki S., A., Masshizaki Y., Kawaji H., Kohtsuki S., Rayashizaki Y., Kawaji H., Kayashizaki Y.
GGSLISPNWVVTAAHCQVTPGRHFVVLGEYDRSSNAEPVQVLSIARAITHPNWNANTMNN 120
                                                        GGSLISENWVVTAAHCGVKT-TDVVVAGEFDQGSDEENVQVLKIAQVFKNPKFNSFTVRN 119
                                                                                                                                                    -i- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPESTN FAMILY.
EMBL; AKO07566; BAB25112.1; -.
HSSP: P00766; IGCT.
                                                                                                                    121 DLTLLKLASPARYTAQVSPVCLASTNEALPSGLTCVTTGWGRISGVGNVTPARLQQVVLP
                                                                                                                                                                                                                                         181 LVTVNQCRQYWGARITDAMICAGGSGASSCQGDSGGPLVCQKGNTWVLIGIVSWGTKNCN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C0638FB8F905A92F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TrEMBLrel. 17, Last sequence update) (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ş
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InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001234; Ser_protease_Try.
InterPro; IPR001254; Ser_protease_Try.
PRINTS; PR00722; CHYMOTRYPSIN.
SMRRT; SW00020; Tryp_SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hydrolase; Serine protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 263 AA;
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=C57BL/65; TISSUE=SPLEEN;

MEDLINE=21085660; PubMed=11217851;

Rawai J., Shinadawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Rawai J., Hara A., Shibata K., Konno H., Adachi J., Fukuda S.,

Arakawa T., Hara A., Shibata K., Konno H., Rasukawa T., Saito T.,

Radota K., Matsuda H.A., Ashburner M., Baralaov S., Casawant T.,

Radota K., Matsuda H.A., Ashburner M., Baralaov S., Casawant T.,

Radota K., Matsuda H.A., Ashburner M., Baralov S., Casawant T.,

Ruchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Ouackenbush J.,

Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washlo T.,

Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Nordone P., Ring B., Ringwald K.H., Weitz C., Whittaker C., Willming L.,

Nordone P., Ring B., Ringwald K.H., Weitz C., Whittaker C., Wilming L.,

Nordone P., Ranganis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Nordone P., Kanda K., Schoenbach C., Schoenbach C., Schoenbach C., Schoenbach C., Schoenbach C., Warahail H., Kohtsuki S.,

Nordone P., Kanda K., Rangawa Y., Kawaji H., Kohtsuki S.,

Nordone P., Kanda K., Rangawa Y., Kawaji H., Kawaji H., Kawaki S.,
190 YWGAR-ITDAMICAGGSGASSCQGDSGGPLVCQKGNTWVLIGIVSWGTKNCNIQAPAMYT 248
                                                                                                                                          110 HPNWNA-NTMNNDLTLLKLASP-ARYTAQVSPVCLASTNEALPSGLTCVTTGWGRISGVG 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     130 VLGTNVSPVCLGESSDVFAPGMKCVTSGWGLTRYNAPG--TPNKLQQAALPLMSNEECSQ
                                                    RYTAQVSPVCLASTNEALPSGLTCVTTGWG--RISGVGNVTPARLQQVVLPLVTVNQCRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17707 MW; 83791FD829ABEDD6 CRC64;
                                                                                                                                                                                                                                                                                                                                                      1-JUN-2001 (TrEMBLrel. 17, Created)
1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47.5%; Score 674; DB 11;
82.2%; Pred. No. 1.7e-52;
                                                                                                                                                                                                                                                                                                                    164 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGD; MGI:88558; Ctrl.
InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00089; trypsin; 1.
PROSITE; P550240; TRYPSIN_DOM; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 409:685-690(2001).
EMBL; AK003074; BAB22549.1;
HSSP; P00763; 1DPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hydrolase; Serine protease.
SEQUENCE 164 AA; 17707 M
                                                                                                                                                                                                                 ||:: |::| |
RVTELRGWVDQILAAN 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 82.2
Matches 129; Conservative
                                                                                                                                                                                               RVSKFSTWINQVMAYN 264
                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                        0910001G08Rik protein.
CTRL OR 0910001G08RIK.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . 997;
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                                                                                                                                                                                                                                                                                                                                                     01-JUN-2001
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEROPS;
                                                                                                                                                                                                                                                                                                                      Q9DC82
                                                                                                                                                                                               249
                                                                                                                                                                                                                                248
                                                                                                                                                                                                                                                                                   RESULT 11
Q9DC82
                                                                                                                                                           qq
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                                                                                                                                                              121 DLTLLKLASPARYTAQVSPVCLASTNEALPSGLTCVTTGWGRISGVGNVTPARLQQVVLP 180
                                                                                                                                                                                                                                  181 LVTVNQCRQYWGARITDAMICAGGSGASSCQGDSGGPLVCQKGNTWVLIGIVSWGTKNCN 240
                                                                                                                                          GGSLISPNWVVTAAHCQVTPGRHFVVLGEYDRSSNAEPVQVLSIARAITHPNWNANTMNN 120
                                                                                                                                                                                                                                                                                                   180 IVSEAKCKESWGSKITDVWICAGASGVSSCMGDSGGPLVCQKDGVWTLAGIVSWGSGFCS 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73 AAHCQVTPGRHFVVLGEYDRS-SNAEPVQVLSIARAITHPNWNANTMNNDLTLLKLASPA 131
                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 ISAAYGCGSPAIQPQVTGYARIVNGEEAVPHSWPWQVSLQQSNGFHFCGGSLINENWVVT 70
                                                                     1 MLLLSLTLSLVLLGSSWGCGVPAITPALSYNQRIVNGENAVPGSWPWQVSLQDNTGFHFC 60
                                                                                         13 LGSSWGCGVPAITPALSYNQRIVNGENAVPGSWPWQVSLQDNTGFHFCGGSLISPNWVVT 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Gadus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 263;
 Length 263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65; Indels
                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHYMOTRYPSIN B. FF61B18A34EE5E7C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAR-2002 (TrEMBLrel. 20, Last annotation update)
Chymotrypsin B precursor (EC 34.21.1).
DB 11;
   .5;
1.6e-62;
78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 758.5; DB 1 Pred. No. 9.1e-60;
                ; Pred. No. 1.6e
41; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47; Mismatches
 55.7%; Score 789.5; 54.5%; Pred. No. 1.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PERMITS: PRO0089; trypsin; 1.
PRINTS: PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPC: 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
PROSITE; PS00135; TRYPSIN_SER; 1.
Hydrolase; Serine profease; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Interpro; IPR001314; Chymotrypsin.
Interpro; IPR001254; Ser_protease_fry.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                            240 TSTPAVYARVTALMPWVQEILEAN 263
                                                                                                                                                                                                                                                                                                                                                      241 IQAPAMYTRVSKFSTWINQVMAYN 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRYPSIN FAMILY.
EMBL; AJ242521; CAB43766.1; -.
HSSP; P00766; 1CHG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28175 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53.5%;
53.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cod)
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                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gadus morhua (Atlantic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            263 AA;
                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEROPS; S01.152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=8049;
                    Best Local Simi
Matches 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09PW06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09PW06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 10
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Gaps

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|||||||:||:||:|| || | : |||||:|
|CGGSLITPDWVLTAGHCISTSRTYQVVLGEHERGVEEGQEQVIPINAGDLFVHPKWNSMC 116
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                                                                                                                                                                                                                                                                                                                                                                                   RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RA Arawa T., Hara A., Shibata K., Yoshino M., Itoh M., Ishli Y.,
Arawawa T., Hara A., Shibata K., Yoshino M., Itoh M., Ishli Y.,
Arawawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Arawawa T., Tawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Saito T., Okazaki Y., Gojobori T., Bono H., Rasukawa T., Saito R.,
Radota K., Matsuda H.A., Ashburner M., Batalov S., Casvant T.,
RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Ring B., Kochiwa H.,
RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schrim L.M., Staubil F., Suzuki R., Tomita M., Magner L., Washio T.,
RA Shrai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojinga N., Carninol P., de Bonaldo M.F.,
ROWINSTELIN D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
Lyons P., Marchioni L., Mashima M., Rodriquez I., Sakamoto N.,
A Lyons P., Marchioni L., Mashima M., Rodriquez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Whyshizaki Y.,
Hayshizaki Y., Kawaji H., Kohtsuki S.,
NVTPARLQOVVLPLVTVNQCRQYWGARITDAMICAGGSGASSCQGDSGGPLVCQKGNTWV 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Musin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 11; Length 269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39.0%; Score 552.5; DB 11; Length 43.1%; Pred. No. 2.2e-41; ive 43; Mismatches 96; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28904 MW; C543F76957B2A7CE CRC64;
                                                                                                                                                                                                                                                                                                            Created)
Last sequence update)
Last annotation update)
                                                                                                     228 LIGIVSWGTKNCNIQAPAMYTRVSKFSTWINQVMAYN 264
                                                                                                                               PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
PROSITE; PS00135; TRYPSIN_SER; 1.
Hydrolase; Serine protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEROPS; S01.154; -...
MGD; MGI:1915118; Ela3b.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00089; trypsin; I.
                                                                                                                                                                                                                                                                 PRT;
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MEDLINE-21085660; PubMed-11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AK010149; BAB26734.1; -. EMBL; AK009129; BAB26092.1; -.
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                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                      01-JUN-2002 (TrEMBLrel.
2310074F01Rik protein.
ELA3B OR 2310074F01RIK.
                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            269 AA;
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                                                                                                                                                                                                                                                                                         Q9CQ52;
01-JUN-2001
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09CQ52
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ATABLE STRAIN-CSTBL/63; TISSUB-STOWACH;

KNAWAI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Knawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Cochiwa H.,

Radota K., Matsuda Y., Nikaido I., Pesole G., Quackenbush J.,

Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Brownstein M.J., Bult C., Fletcher C., Fullita M., Mariboldi M.,

Ry Saki H., Salo K., Schoenbach C., Sakamoto N.,

Sakai H., Sato K., Schoenbach C., Saya T., Shibata Y., Storch K.-F.,

Suzuki H., Toyo-oka K., Wang K.H., Weltz C., Whittaker C., Wilming L.,

Whyshaw-Bootis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Nordone P., Rung B., Kanga K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Nordone P., Kohtsuki K., Wang K.H., Weltz C., Whittaker C., Wilming L.,

Nordone P., Rung B., Kanga K., Wang K.H., Weltz C., Whittaker C., Wilming L.,

Nordone P., Rung B., Kanga K., Wang K.H., Weltz C., Whittaker C., Wilming L.,

Nordone P., Rung B., Kanga K., Wang K.H., Weltz C., Wawaji H., Kohtsuki S.,

Nordone P., Rung B., Wang K.H., Weltz C., Wawaji H., Kohtsuki S.,

Nordone P., Kang B., Wang K.H., Weltz C., Wawaji H., Kohtsuki S.,

Nordone P., Kang B., Kang B., Wang K.H., Weltz C., Wawaji H., Kohtsuki S.,

Nordone P., Kang B., Wang K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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                                                                                                                                                                                                                                                                                   OVVLPLVTVNQCRQ--YWGARITDAMICAGGSGASSCQGDSGGPLVCQKGN-TWVLIGIV 232
                                                                                                                                                                                                                                                                                                                                                                                                                  176 QALLPVVDYEHCSRWNWWGLSVKTTMVCAGGDIQSGCNGDSGGPLNCPADNGTWQVHGVT 235
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-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Last annotation update)
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InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001234; Ser_protease_Try.
InterPro; IPR001254; Ser_protease_Try.
PRINTS; PR00089; trypsin; 1.
PRINTS; PR00020; Tryp_SPc; 1.
PROSITE; PS50240; TRYPSIN_DM; 1.
PROSITE; PS00134; TRYPSIN_LHS; UNKNOWN_1.
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MEROPS; S01.154; -.
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01-JUN-2001 (TrEMBLrel. 17, C.
01-JUN-2001 (TrEMBLrel. 17, L.
01-JUN-2002 (TrEMBLrel. 21, L.
2310074F01R1 proteân.
ELA3B OR 2310074F01R1K.
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Matches 117; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
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60 CGGSLISPNWVVTAAHCQVTPGRHFVVLGEYDRSSNAEPVQVLSI--ARAITHPNWNANT 117

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117 NDIALIKLASPVDVSAIITPACVPDAEVLLANGAPCYVTGWGRLWTGGPIADA-LQQALL 175
                                                                                                                                                                                                                                                                                    65 ISPNWVVTAAHCQVTPGRHFVVLGEYDRSSNAEPVQVLSIARAITHPNWNANTMNNDLTL 124
                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neoperygii; Teleostei; Neoteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
Pleuronectoidei; Paralichthyidae; Paralichthys.
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MKLLVFALFVAGAYGCGLPTFPPIVT - - - RVVGGEDVRVHSWPWQASLQYKSGNSFYHTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 LSLVLLGSSWGCGVPAITPALSYNQRIVNGENAVPGSWPWQVSLQDNTG---FHFCGGSL
                                                                                                                                                NDLTLLKLASPARYTAQVSPVCLASTNEALPSGLTCVTTGWGRISGVGNVTPARLQQVVL
                                                                                                                                                                                                                                                       PLVTVNQCRQY - - WGARITDAMICAGGSGA - SSCQGDSGGPLVCQKGN - TWVLIGIVSWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Suzuki T., Srivastava A.S., Kurokawa T.;
"Japanese flounder mRNA for elastase 4 precursor.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
-: SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS TRYSIN FAMILY.
EMBL; RABO29758; BAA82370.1; --
HSSP; PO0761; 1EPT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37.0%; Score 524.5; DB 13; Length 260; 40.3%; Pred. No. 6.7e-39; Live 58; Mismatches 84; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      260 AA; 27942 MW; 61883CD1BGA66075 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  260 AA
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SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
PROSITE; PS00135; TRYPSIN_ESF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
                                                                                                                                                                                                                                                                                                                                                                                   236 SSMGCNYPKKPSVFTRVSAYIPWINNW 263
                                                                                                                                                                                                                                                                                                                                                         TK-NCNI-QAPAMYTRVSKFSTWINQVM 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1999 (TrEMBLrel. 12, Create 01-NOV-1999 (TrEMBLrel. 12, Last s 01-MAR-2002 (TrEMBLrel. 20, Last a Elastase 4 (Fragment).

Paralichthys olivaceus (Flounder).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hydrolase; Serine protease.
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Matches 106;
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Q9W7P9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINES-965679; PubMed=8925447; MEDLINES-96562679; PubMed=8925447; Gudmundsdottir E., Spilliaert R., Yang Q., Craik C.S., Bjarnason J.B., Gudmundsdottir A.;
                                                                                                                                                        118 MN--NDLTLLKLASPARYTAQVSPVCLASTNEALPSGLTCVTTGWGRISGVGNVTPARLQ 175
                                                                                                                           60 CGGSLISPNWVVTAAHCQVTPGRHFVVLGEYDRSSNAEPVQVLSI--ARAITHPNWNANT 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gadus morhua (Atlantic cod).

Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Gadus.
                                                                                                                                                                                                                                                                                                                                                           01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NUN-2002 (TrEMBLrel. 21, Last annotation update)
Elastase precursor (EC 3.4.21.37) (Leukocyte elastase) (Lysosomal elastase) (Neutrophil elastase) (Bone marrow serine protease)
                                                    "Isolation and characterization of two cDNAs from Atlantic cod encoding two distinct psychrophilic elastases.";
Comp. Biochem. Physiol. 113B:795-801 (1996).
-i- CATALYTIC ACTIVITY: HYDROLYSIS OF PROTEINS, INCLUDING ELASTIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PREFERENTIAL CLEAVAGE: VAL-|-XAA > ALA-|-XAA.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
                            LLSLTLSLVLLGSSWGCGVPAITPALSYNQRIVNGENAVPGSWPWQVSLQ---DNTGFHF
                                                                                                                                                                                                                                                                               117 VSCGNDIALVKLSRSAQLGDAVQLACLPPAGEILPNGAPCYISGWGRLSTNGPL-PDKLQ
                                                                                                                                                                                                                                                                                                                            176 QVVLPLVTVNQCRQ--YWGARITDAMICAGGSGASSCQGDSGGPLVCQKGN-TWVLIGIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15;
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SIGNAL 1 15 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                236 SFVSSLGCNTLRKPTVFTRVSAFIDWIEETIANN 269
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InterPro: IPRO01314; Chymotrypsin.
InterPro: IPRO01214; Ser_protease_Try.
Pfam: PF00089; trypsin. 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SMO020; Tryp.SPC: 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_LES; UNKNOWN_1.
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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
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Post-processing: Minimum Match 0% Maximum Match 100% . Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score		% Query Match Length DB ID	DB	ID	Description
-	1418	!	264	21	AAB11711	Mouse serine prote
7	1262			21	AAB11710	Human serine prote
m	889		192	21	AAB54077	Human pancreatic c
4	822.5			23	AAU82738	Amino acid sequenc
5	774.5			21	AAY99596	Bovine chymotrypsi
9	755.5			22	AAB98504	Human chymotrypsin
7	537			7	AAP61724	Porcine elastase I
80	537			œ	AAP70758	Pig pancreas elast
σ	523.5			13	AAR29621	Porcine pancreatic
10	515			7	AAP60062	Sequence of human

98JP-0347806.

19-NOV-1999; 20-NOV-1998;

02-JUN-2000

WO200031243-A1

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The invention relates to novel serine proteases designated BSSP5

(AABI1710-B11711), and to nucleic acids encoding them (AAA61733-A61734).

The invention also relates to vectors and transformants comparising BSSP5
nucleic acids; transgenic animals in which the expression level of BSSP5
nucleic acids; transgenic animals in which the expression level of BSSP5
can be varied; and an mBSSP5 knockout mouse. The invention additionally
antibodies, methods of BSSP5 antibodies and methods of production of such
medical conditions, e.g., pancreatist as diagnostic markers for certain
medical conditions or fragments as diagnostic markers for certain
medical conditions, e.g., pancreatitis. A method for detecting
ancreatitis comprising measuring BSSP5 concentration in the blood or
urine, and a pancreatitis diagnostic agent containing an anti-BSSP5
curine, and splo disclosed. Nucleotides encoding BSSP5 were initially
isolated in a human brain cDNA library using degenerate PCR primers
(AAA6174-A61745) based on conserved regions of serine proteases. The
BSSP5 serine proteases and nuclectides encoding them are useful in
detecting homologues, mutants and polymorphic variants in biological
samples (e.g., blood, urine, brain, prostate gland, placenta, teetis,
pancreas and spleen) as diagnostic markers for conditions such as
Alzheimer's disease, epilepsy, cancer, inflammation, infertility,
pancreatitis and prostatic hypertrophy. Sequence AAB11711 represents murine BSSP5
chuman BSSP5
characteric proper account and sequence AAB11711 represents
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polymorphic variants as markers for diagnosis of e.g. Alzheimer's disease, epilepsy, cancer and inflammation, using blood, urine, pancreas or other tissues
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                                                                                            Claim 3; Page 55-56; 70pp; Japanese.
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The invention letaces to novel settine proceases designated bases.

The invention also relates to vectors and transformants comprising BSSP5 nucleic acids; transgenic animals in which the expression level of BSSP5 cucleids; transgenic animals in which the expression level of BSSP5 cucleids; transgenic animals in which the expression level of BSSP5 cucleids and am mBSSP5 knockout mouse. The invention additionally encompasses anti-BSSP5 antibodies and methods of production of such antibodies, methods of BSSP5 detection using the antibodies, and the use of BSSP5 proteins or fragments as diagnostic markers for certain medical conditions, e.g., pancreatitis. A method for detecting comprising measuring BSSP5 concentration in the blood or urine, and a pancreatitis diagnostic agent containing an anti-BSSP5 antibody is also disclosed. Nucleotides encoding BSSP5 were initially isolated in a human brain orNA library using degenerate PCR primers (AAA6174-A61745) based on conserved regions of serine proteases. The BSSP5 serine proteases and nucleotides encoding them are useful in the BSSP5 serine proteases and nucleotides encoding them are useful in samples (e.g., blood, urine, brain, prostate gland, placenta, testis, pancreas and spleen) as diagnostic markers for conditions such as alreading and prostatic hypertrophy. Sequence AAB1171 represents murine BSSP5 human BSSP5 (hBSSP5), and sequence AAB1171 represents murine BSSP5).
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                                                                                                                                                                                                                                                                                                                          Serine proteases BSSP5, useful in detecting homologs, mutants and polymorphic variants as markers for diagnosis of e.g. Alzheimer's disease, epilepsy, cancer and inflammation, using blood, urine, pancreas or other tissues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to novel serine proteases designated BSSP5
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                                                                                                                                                                                                                    Yamaguchi N,
                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 51-52; 70pp; Japanese.
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Consideration of the human pancreatic cancer antigens have cytostatic, contraceptive, neuroprotective, neotropic, immunomodulatory, relaxant, contraceptive, gynaecological, cardiant and antilifammatory activities, and can be used in gene therapy. The polynucleotide and proteins can be used for preventing, treating, or ameliorating a medical condition or in assays for diagnosing a pathological condition or a susceptibility to one in a subject. Binding partners to the proteins and the activity of the proteins can be identified. The pancreatic cancer antigens can be used to detect, treat or prevent pancreatic disorders, especially cancer.

Consideratic cancer antigen polynucleotides can be used to design nucleic actd hybridisation probes that can be used in chromosome mapping, linkage and hybridisation probes that can be used to generate antibodies and diagnostic methods. The proteins can be used to generate antibodies which are used to purify, detect and target the polypeptides, including the proteins can be the protein methods. The proteins can diagnostic methods. The proteins can diagnostic methods. The proteins can diagnostic methods. The proteins can diagnostic methods. The proteins can diagnostic methods. The proteins can diagnostic methods. The proteins can diagnostic methods. The proteins can diagnostic methods. The proteins can diagnostic methods. The proteins can diagnostic methods. The proteins can diagnostic methods. The proteins can be used to generate antiboding the polyment of the cancer cancer antiboding the content of the cancer cancer cancer cancer cancer cancer cancer cancer cancer cancer cancer cancer cancer cancer cancer cancer cancer cancer cancer cancer cancer cancer cancer cancer cancer cancer cancer cancer cancer cancer cancer cancer cancer cancer cancer cancer cancer cancer cancer cancer cancer cancer cancer cancer cancer cancer cancer cancer cancer cancer can
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; pancreas; pancreatic cancer; pancreatic cancer antigen; detection; diagnosis; identification; offsettic; neuroprotective; nootropic; immunomodulatory; relaxant; contraceptive; gynaecological; antiinflammatory; cardiant; gene therapy; chromosome mapping; linkage analysis; itssue identification; tissue typing; forensic; neural; immune system; muscular; reproductive; gastrointestinal; pulmonary; cardiovascular; renal; proliferative.
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                                                                                                                                                                                                                                                                                                                                                                        Human pancreatic cancer antigen protein sequence SEQ ID NO:529.
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                                             AAB54077 standard; Protein; 192 AA
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AAB54077
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The present invention relates to the isolation of novel human proteases, and the nucleic acids encoding them. The sequences of proteases, and the nucleic acids encoding them. The sequences of the invention are useful for treating diseases and disorders such as cancers (e.g. breast, colon, lung), immune-related diseases and disorders (e.g. inflammatory diseases and asthma), cardiovascular diseases (e.g. inflammatory disorders (e.g. disorders), brain or neuronal-associated diseases, metabolic disorders (e.g. diabetes, obesity), inflammatory disorders (e.g. rheumatoid arthritis and postiasis), central or peripheral nervous system diseases, migraines, pain, sexual dysfunction, mood disorders, attention disorders, neurological disorders, hypotension, hypertension, psychotic disorders, neurological disorders (e.g. Alzheimer's disease, Parkinson's disease) and dyskinesias.

The nucleic acids and polypeptides are also useful for treating viral infections caused by human immunodeficiency virus (HIV), and non-viral infections such as ocular disease (e.g. glaucoma) and macular checked in the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the con
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                            Nucleic acids encoding novel human proteases, useful for useful for treating diseases and disorders such as cancers, immune-related diseases and disorders, cardiovascular disease (e.g. restenosis) and inflammatory disorders
  LKLASPARYTAQVSPVCLASTNEALPSGLTCVTTGWGRISGVGNVTPARLQQVVLPPLVTV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Amino acid sequence of novel human protease #37.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ocular disease; cytostatic; enzyme.
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N-PSDB; ABK31780.
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                                                                                                                                             NOCROYWGS 189
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Charydczak G;
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                                                                                                          185
                                                      121
                                                                                                                                                              181
125
                                                                                                                                                                                                                                               RESULT 4
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Gaps

SLTLSLVLLGSSWGCGVPAITPALSYNQRIVNGENAVPGSWPWQVSLQDNTGFHFCGGSL 64

Conservative

al Similarity 160; Conserv

Local Best Loca Matches

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QTLAAN 245
                                                                                                                                                                                                                                                                                                                                                                                                      QVMAYN 264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ovarian cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-0CT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             O'Brien TJ,
                                                                                               Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB98504;
                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human;
                                                                                                                                                                                                                                                                                                                                                                                                                              240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ношо
                                                                                                                                                                                                                                                               61
                                                                                                                                                                                                                                                                                                                                                                                                      259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB98504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       888888888
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                                                       1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polypeptide with plasminogen activator activity useful as thrombolytic agent for treating blood clot disorders e.g. heart attack, comprises 10 amino acid peptide fragment for recognition or activation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is bovine chymotrypsinogen. It was included in a review of sequence homologies of several plasminogen activators. Plasminogen is the principal series protease zymogen in the extracellular fluids of vertebrates. Its active form, plasmin, is implicated in pericellular proteolysis associated with a wide range of physiological and pathological processes. Plasminogen expression is regulated by plasminogen activators which hydrolyse a peptide bond in plasminogen to convert it to plasmin or form tight binding complexes with plasminogen to spontaneously convert it to plasmin. The sequence homology analysis has identified a six amino acid peptide involved in
                                                                                                                                                      181 LVTVNQCRQYWGARITDAMICAGGSGASSCQGDSGGPLVCQKGNTWVLIGIVSWGTKNCN 240
                                                                                                                                      GGSLISPNWVVTAAHCQVTPGRHFVVLGEYDRSSNAEPVQVLSIARAITHPNWNANTMNN 120
                                                       Gaps
                                                                                                           9
                                                                                 MLLLSLTLSLVLLGSSWGCGVPAITPALSYNORIVNGENAVPGSWPWQVSLQDNTGFHFC 60
                                                                                               DLTLLKLASPARYTAQVSPVCLASTNEALPSGLTCVTTGWGRISGVGNVTPARLQQVVLP
                                                     ij
                           Length 263;
                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cardiant; thrombolytic;
                             ..5e-61;
73;
                          DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               heart attack; stroke; blood clotting disorder
                                                       Mismatches
                          Score 822.5;
Pred. No. 1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 35-36; 41pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (OKLA-) OKLAHOMA MEDICAL RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                       AA.
                                                                                                                                                                                                                                                                                                         241 IQAPAMYTRVSKFSTWINQVMAYN 264
                                                                                                                                                                                                                                                                                                                                   240 TTTPAVYARVTKLIPWVQKILAAN 263
                                                                                                                                                                                                                                                                                                                                                                                                      AAY99596 standard; protein; 245
                                                     39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  plasminogen activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tang JJN;
                           58.0%;
57.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99WO-US09991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98US-0110588
                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bovine chymotrypsinogen A.
                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-422975/36.
                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zhang XC,
 263 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200032759-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               plasminogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bos taurus
                                                       151;
                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY99596;
 Sequence
                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bovine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lin X,
                                                       Matches
                                                                                                                                        61
                                                                                                                                                                  61
                                                                                                                                                                                             121
                                                                                                                                                                                                                                                                                                                                                                           RESULT 5
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plasminogen activation. This peptide is particularly useful when inserted between amino acid residues 644 and 645 of full length human plasminogen. Novel plasminogen activators have been made based upon the plasminogen activation/recognition site of plasminogen binding proteins. The polypeptides are useful in preparing thrombolytic agents for treating blood clotting disorders such as heart attack.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to human tumour antigen-derived gene 15 (TADG-15) protein and coding sequence (see AAH23601 and AAB98500). TADG-15 is an extracellular serine protease. It was found that TADG-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel extracellular serine protease, termed tumor antigen-derived gene 15 protein overexpressed in carcinomas and DNA encoding it, for diagnosis, treatment, prevention of cancer, particularly breast,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79 TPGRHFVVLGEYDRSSNAEPVQVLSIARAITHPNWNANTMNNDLTLLKLASPARYTAQVS 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     139 PVCLASTNEALPSGLTCVTTGWGRISGVGNVTPARLQQVVLPLVTVNQCRQYWGARITDA 198
                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                      78
                                                                                                                                                                                                                                                                                                                                                                                         19 CGVPAITPALSYNQRIVNGENAVPGSWPWQVSLQDNTGFHFCGGSLISPNWVVTAAHCQV
                                                                                                                                                                                                                                                                                                                                                                                                                    1 CGVPAIQPVLSGLSRIVNGEEAVPGSWPWQVSLQDKTGFHFCGGSLINENWVVTAAHCGV
                                                                                                                                                                                                                                                                                                                               1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; TADG-15; cytostatic; vaccine; ovarian tumour; cancer;
tumour antigen-derived gene 15; serine protease; chymotrypsin.
                                                                                                                                                                                                                                                                   Length 245;
                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human chymotrypsin serine protease catalytic domain.
                                                                                                                                                                                                                                                                      DB 21;
                                                                                                                                                                                                                                                                                                                               72;
                                                                                                                                                                                                                                                                54.6%; Score 774.5; DB: 57.3%; Pred. No. 1.6e-57.ive 32; Mismatches 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ¥.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB98504 standard; Protein; 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0421213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                  Matches 141; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ξ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UYAR-) UNIV ARKANSAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-381031/40.
                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                245 AA;
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59 FCGGSLISPNWVVTAAHCQVTPGRHFVVLGEYDRSSNAEPVQVLSIARAITHPNWNANTM 118
                                                                     119 N--NDLTLLKLASPARYTAQVSPVCLASTNEALPSGLTCVTTGWGRISGVGNVTPARLQQ 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 LLLSLTLSLVLLGSSWGCGVPAITPALSYNQRIVNGENAVPGSWPWQVSLQ-DNTG--FH 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence encoding pancreas elastase may be used to transform an expression system. The product is useful in reluvenating the elasticity of the arterial wall, and improving unusual serum lipid levels and lipoprotein metabolism.
                   177 VVLPLVTVNQCRQ--YWGARITDAMICAGGSG-ASSCQGDSGGPLVCQKGN-TWVLIGIV
     2 LLLSLTLSLTLSLVLLGSSWGCGVPAITPALSYNQRIVNGENAVPGSWPWQVSLQ-DNTG--FH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pancreas elastase prodn. used to improve lipoprotein metabolism comprises isolating RNA coding elastase, synthesising single and double chain cDNA and introducing recombinant into host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37.9%; Score 537; DB 8; Length 269;
43.1%; Pred. No. 2e-37;
tive 48; Mismatches 92; Indels
                                                                                                                                                                                                               SWGTK-NCN-IQAPAMYTRVSKFSTWINQVMAYN 264
                                                                                                                                                                                                                              |:|: || |::||| |:::|||| |:| |SFGSSLGCNYYHKPSVFTRVSNYIDWINSVIANN 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
2..16
/note= "May be absent"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 480; 18pp; Japanese.
                                                                                                                                                                                                                                                                                                            Æ
                                                                                                                                                                                                                                                                                                          AAP70758 standard; Protein; 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48;
                                                                                                                                                                                                                                                                                                                                                                                                                  Lipoprotein metabolism; lipid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85JP-0138494
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                                                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                        Pig pancreas elastase-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1987-040875/06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        269 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference
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                                                                                                                                                                                                                                                                                                                                                              19-APR-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Sus scrofa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Sin
Matches 118;
                                                                                                                                                                                                                                                                                                                                   AAP70758;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                     176
                                                                                                                                                                                                               233
                                                                                                                                                                                                                                         236
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over-expressed in ovarian tumours. TADG-15 protein or its fragments of 9-20 residues that lack TADG-15 protease activity are useful for vaccinating an individual against TADG-15, having, suspected of having or at risk of getting cancer. Furthermore, the TADG-15 gene can be used as a diagnostic or therapeutic target in cancer. The present sequence was used in a sequence homology alignment with the catalytic domain of TADG-15.
                                                                                                                                                                                                                                                                                             SSNAEPVQVLSIARAITHPNWNANTMNNDLTLLKLASPARYTAQVSPVCLASTNEALPSG 152
                                                                                                                                                                                                                                                                              153 LTCVTTGWGRISGVGNVTPARLQQVVLPLVTVNQCRQYWGARITDAMICAGGSGASSCQG 212
                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                      33 RIVNGENAVPGSWPWQVSLQDNTGFHFCGGSLISPNWVVTAAHCQVTPGRHFVVLGEYDR 92
                                                                                                                                                                                     The porcine elastase product may be efficiently expressed from a transformed host such as collbacillus or yeast, yielding the product more efficiently than spleen extraction.
                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16;
                                                                                                                     Length 231;
                                                                                                                                                                                                                                                                                                                                                DSGGPLVCQKGNTWVLIGIVSWGTKNCNIQAPAMYTRVSKFSTWINQVMAYN 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biological prepn. of pig elastase II - using DNA with base sequence coding for specified aminoacid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37.9%; Score 537; DB 7; Length 26
43.1%; Pred. No. 2e-37;
:1ve 48; Mismatches 92; Indels
                                                                                                                                                61; Indels
                                                                                                                   DB 22;
                                                                                                                  53.3%; Score 755.5; DB 2
58.2%; Pred. No. 5.8e-56;
iive 35; Mismatches 61
                                                                                                                                                                                                                                                                                                                                                                                                                          AAP61724 standard; Protein; 269 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Fig 1; 11pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 43.1
Matches 118; Conservative
                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (KIRI ) KIRIN BREWERY KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Porcine elastase II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Colibacillus; yeast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1986-262895/40.
                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              See also J61192288
                                                                                           231 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        269 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAN60919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JP61192289-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-FEB-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-FEB-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-OCT-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-AUG-1986
                                                                                                                                               135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sus scrofa.
                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAP61724;
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                                                                                                                   Query Match
Best Local
                                                                                                                                               Matches
                                                                                                                                                                                                                           93
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190 YWGARITDAMICAGGSGASSCQGDSGGPLVCQKGN-TWVLIGIVSW-GTKNCN-IQAPAM 246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FCGGSLISPNWVVTAAHCQVTPGRHFVVLGEYDRSSNAEPVQVLSIARAITHPNWNANTM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N--NDLTLLKLASPARYTAQVSPVCLASTNEALPSGLTCVTTGWGRISGVGNVTPARLQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        177 VVLPLVTVNQCRQ--YWGARITDAMICAGGSGA-SSCQGDSGGPLVCQKGN-TWVLIGIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The genetically engineered prod. can eliminate the dependency on human pancreas supplies for the elastase, and avoids antibody formation and possibility of anaphylaxis using porcine elastase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 36.3%; Score 515; DB 7; Length 269; Best Local Similarity 41.6%; Pred. No. 1.4e-35; Matches 114; Conservative 47; Mismatches 97; Indels 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          elastase - obtd
                                                                                                                                                                                                                                        Sequence of human pancreatic elastase IIA encoded on pH2E2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ohmine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eurukawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New genetically engineered human pancreatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       using hosts modified DNA coding for enzyme
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                                                                                                                                                                                                                                                                  Enzyme; serum lipoprotein metabolism
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                                                                                                                                                     AAP60062 standard; Protein; 269
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85JP-0091986.
85JP-0163964.
85JP-0271128.
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                                                                                                                                                                                                             (first entry)
                                                     YTRVSKFSTWINGVMA 262
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FTRTSAFIDWIEEIIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Takiguchi Y, Tani T,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    269 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SANY ) SANKYO KK.
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                                                                                                                                                                                                                                                                                              Homo sapiens
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27-APR-1985;
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                                                                                                                                                                                 AAP60062;
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                                                                    FCGGSLISPNWVVTAAHCQVTPGRHFVVLGEYDRSSNAEPVQVLSIARAITHPNWNANTM 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CQVTPGRHFVVLGEYDRSSNAEPVQVLSI -- ARAITHPNWNANTMN -- NDLTLLKLASPA 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56
                                                                                                                                                                                                                                                                                                                                                                            swine; bile acid; gall bladder; bile acid secretion promoters;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents porcine pancreatic elastase III. It was expressed in E. coli YA21 using the expression vector pELE001. It may be used in bile acid secretion promoters and liver function
             CGVPAITPALSYNQRIVNGENAVPGSWPWQVSLQ-DNTGF--HFCGGSLISPNWVVTAAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CISSSLIYQVVLGEYDRSENEGFEQVIPINAGDLFVHPRWNSNCVSCGNDIALVKLSRSA
                                                    N--NDLTLLKLASPARYTAQVSPVCLASTNEALPSGLTCVTTGWGRISGVGNVTPARLQQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pig pancreas elastase protein - used in bile acid secretion
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86;
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llarity 43.0%; Pred. No. 2.56
Conservative 43; Mismatches
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                                                                                                                                                                                                                                                                                                                                                  Porcine pancreatic elastase III.
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                                                                                                                                                                                                                                                               AAR29621 standard; Protein; 253
                                                                                                                                                                                                                                                                                                                                                                                            liver function improvers; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                        Sus scrofa domestica.
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Best Local Similarity
Matches 110; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           253 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAQ31724
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Gaps 28

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N -- NDLTLLKLASPARYTAQVSPVCLASTNEALPSGLTCVTTGWGRISGVGNVTPARLQQ 176
                                                                                                                                                            The human elastase product may be efficiently expressed from a transformed host such as collbacillus or yeast, yielding the product more efficiently than spleen extraction. See also J61192289.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59 FCGGSLISPNWVVTAAHCQVTPGRHFVVLGEYDRSSNAEPVQVLSIARAITHPNWNANTM 118
                                                        FCGGSLISPNWVVTAAHC----QVTPGRHFVVLGEYDRSSNAEPVQVLSIARAITHP 111
                                                                                                                                     NWNANTMN--NDLTLLKLASPARYTAQVSPVCLASTNEALPSGLTCVTTGWGRISGVGNV 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              170 TPARLOQVVLPLVTVNQCRQ--YWGARITDAMICAGGSGA-SSCQGDSGGPLVCQKGNT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LLLSLTLSLVLLGSSWGCGVPAITPALSYNQRIVNGENAVPGSWPWQVSLQDNTG---FH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biologically producing human elastase ii – using DNA chain with biological prodn. capability for human elastase II.
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                                                                                                                                                                                                                                                                                                                       239 WQVHGIVSFGSRLGCNYYHKPSVFTRVSNYIDWINSVIAYN 279
                                                                                                                                                                                                                                                                                                  WVLIGIVSWGTK-NCN-IQAPAMYTRVSKFSTWINQVMAYN 264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Colibacillus; yeast
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human elastase II
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving considers in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating the polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations considers in the constant of the polypeptide and polynucleotide sequences have applications in diagnostics.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wIpo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                   Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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                                     45; Mismatches
              SWGTK-NCN-IQAPAMYTRVSKFSTWINQVMAYN 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 20; SEQ ID No 50872; 103pp; English.
                                                                                                                                                                                                                                                                           Novel human diagnostic protein #20504.
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                                                                                                                                                      ABG20513 standard; Protein; 279
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23-AUG-2000; 2000US-0649167.
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Matches 112; Conservative
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N-PSDB; AAS84700.
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                                                                                                                                                                                                                                                                                                                                                                                                                   WO200175067-A2
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59 CGGTLIASNFVLTAAAHCISNTXTYRVAVGKNNLEVEDEEGSLFVGVDTIHVHKRWNALLL 118
                                                119 NNDLTLLKLASPARYTAQVSPVCLASTNEALPSGLTCVTTGWGRISGVGNVTPARLQQVV 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | : : | | | : : | | | :: CISSSRTYRVGLGRHNLYVAESGSLAVSVSKIVVHKDWNSNQISKGNDIALLKLANPVSL 117
                                                                                                            179 LPLVTVNQCRQ--YWGARITDAMICAGGSGA-SSCQGDSGGPLVCQKGN-TWVLIGIVSW 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76 CQVTPGRHFVVLGEYDRSSNAEPVQVLSIARAITHPNWNANTMN--NDLTLLKLASPARY 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19 CGVPAITPALSYNQRIVNGENAVPGSWPWQVSLQDNTG---FHFCGGSLISPNWVVTAAH 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The genetically engineered prod. can eliminate the dependency on human pancreas supplies for the elastase, and avoids antibody formation and possibility of anaphylaxis using porcine elastase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ohmine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human pancreatic elastase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New genetically engineered human pancreationsing hosts modified DNA coding for enzyme
                                                                                                                                                                                                                                                                                                                                                                                Sequence of human pancreatic elastase IIA.
                                                                                                                                                                           235 GT-KNCNI-QAPAMYTRVSKFSTWINQVM 261
                                                                                                                                                                                           Enzyme; serum lipoprotein metabolism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kawashima I,
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85JP-0072308.
85JP-0091986.
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85JP-0271128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1986-280300/43.
N-PSDB; AAN60072.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                252 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Takiguchi Y,
Ohsumi J;
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27-APR-1985;
26-JUL-1985;
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SKGNDIALLKLANPVSLTDKIQLACLPPAGTILPNNYPCYVTGWGRLQTNGAV-PDVLQQ 175
                                177 VVLPLVTVNQCRQ--YWGARITDAMICAGGSGA-SSCQGDSGGPLVCQKGNTWVLI-GIV 232
                                                60 CGGSLISPNWVVTAAHCQVTPGRHFVVLGEYD-RSSNAEPVQVLSIARAITHPNWNANTM 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human caldecrin preprosequence is encoded by AAT15536. Expression vectors contg. the DNA can be used for the recombinant production of caldecrin from transformant host cells. The caldecrin is used as a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 LLSLTLSLVLLGSSWGCGVPAITPALSYNQRIVNGENAVPGSWPWQVSLQ---DNTGFHF 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35.0%; Score 496.5; DB 17; Length 40.1%; Pred. No. 5.2e-34; Live 46; Mismatches 102; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA encoding rat and human caldecrin and related vectors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    caldecrin for use as serum calcium lowering agent
                                                                                                                                                                                                                                                                                                                              human; calcium serum lowering agent;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tomomura A;
                                                                                                               SWGTK-NCN-IQAPAMYTRVSKFSTWINQVMAYN 264
                                                                                                                                                                                                                                                                                                                                                                                                                                           'label - pre-pro-sequence
                                                                                                                                                                                                                                                                                                                                                  recombinant production; preproseguence.
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                                                                                                                                                                                                                                                                                                 Human caldecrin contg. preprosequence
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nes 108; Conservative
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30..268
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24-JUN-1994;
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                                                                                                                                                                                                                                                                                                                                 caldecrin;
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Key Peptide Peptide Protein 10;

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Query Match

Matches

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               RYTAQVSPVCLASTNEALPSGLTCVTTGWGRISGVGNVTPARLQOVVLPLVTVNQCRQY- 190
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                                                192 GARITDAMICAGGSGA-SSCQGDSGGPLVCQKGN-TWVLIGIVSWGTK-NCN-IQAPAMY 247
TAQVSPVCLASTNEALPSGLTCVTTGWGRISGVGNVTPARLQQVVLPLVTVNQCRQ--YW 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34.4%; Score 487.5; DB 12; Length 811;
40.9%; Pred. No. 1.1e-32;
tive 31; Mismatches 104; Indels 17; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16 SWGCGVPAITPALSYNQRIVNGENAVPGSWPWQVSLQDNTGFHFCGGSLISPNWVVTAAH 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This protein is a plasminogen mutant cleavable by Factor Xa. Activation is localised to the thrombus because cleavage to plasmin is by an enzyme of the blood clotting pathway. Compositions comprising the mutant plasminogen are used for treatment or prevention of thrombosis, etc.

See AAQ12543-Q12558.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Activatable fibrinolytic and antithrombic proteins - activated e.g. factor \rm Xa , thrombin or activated protein \rm C
                                                                                                                                                                                                                                                               Plasminogen mutein X1 with factor Xa cleavage site.
                                                                                                                                                                                                                                                                                        protease; fibrinolysis; blood clotting; thrombosis
                                                                                                                                                                                                                                                                                                                Location/Qualifiers
578..581
/label= Factor Xa cleavage site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 7; Fig 2 and Fig 4; 73pp; English.
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                                                                                                                                                                                      AAR12933 standard; Protein; 811 AA
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90WO-GB01911.
                                                                                                              (BRBI-) BRIT BIO-TECHN LTD
                                                                                               248 TRVSKFSTWINOVMAYN 264
                                                                                                                                                                                                                                        (first entry)
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Matches 105; Conservative
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N-PSDB; AAQ12542.
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07-DEC-1990;
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Search completed: December 20, 2002, 15:16:41 Job time : 42.6957 secs

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GenCore version 5.1.3
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 protein search, using sw model OM protein

December 20, 2002, 15:16:49 ; Search time 7.30435 Seconds (without alignments) 530.147 Million cell updates/sec Run on:

Title: Perfect score:

US-09-856-319B-2_COPY_1_231 1221 1 MLLLSLTLSLVLLGSSWGCG.......GDSGGPLVCQKGNTWVLIGI 231 Sequence:

Scoring table:

106657 seqs, 16763532 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

106657

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Published_Applications_AA:* Database :

1: / cgn2_6/ptodata/1/pubpaa/USOB_NEW_PUB.pep:*
2: / cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
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4: / cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
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12: / cgn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*
13: / cgn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*
13: / cgn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*
14: / cgn2_6/ptodata/1/pubpaa/USO0_NEW_PUB.pep:* 

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	l Query Match Length DB	DB	ID	Description
1	966	81.6	192	101	US-09-925-297-529	Sequence 529, App
7	684.5	56.1	263	10	US-09-888-615-96	96.
m	427.5	35.0	269	10	US-09-925-297-576	
4	420.5	34.4	270	10	US-09-923-779-152	152, 7
S	420.5	34.4	273	10	US-09-925-297-695	Sequence 695, App
9	410.5	33.6	343	10	US-09-948-094-2	Sequence 2, Appli
7	408.5	33.5	453	6	US-09-978-295A-69	Sequence 69, Appl
80	408.5	33.5	453	0	08-09-978-697-69	
6	408.5	33.5	453	σ	US-09-978-192A-69	-
10	408.5	33.5	453	12	US-10-052-586-64	•
11	408	33.4	248	10	US-09-925-301-1017	~
12	408	33.4	327	10	US-09-804-156-16	Sequence 16, Appl
13	408	33.4	327	10	US-09-946-633-8	Sequence 8, Appli
14	408	33.4	454	10	US-09-888-615-103	Sequence 103, App
15	397	32.5	791	6	US-09-967-386-1	Sequence 1, Appli
16	397	32.5	810	10	US-09-946-893-2	
17	389.5	31.9	812	σ	US-09-335-325-1	Sequence 1, Appli
18	389.5	31.9	812	10	US-09-788-142-1	
19	389.5	31.9	812	10	US-09-761-120-1	Sequence 1, Appli

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25-297-643 88-975A-6 88-975A-6 88-975A-6 88-975A-6 88-975A-6 88-975A-6 88-975A-6 88-975A-6 88-975A-6 88-975A-6 88-975A-6 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934 88-975-934	Score 996; DB 10; Length Pred. No. 8.4e-83; 0; Mismatches 1; Indel	SLTLSLVLLGSSWGCGIPAIKPALSFSQRIVNGENAVLGSWPWQVSLQDSSGFHFCGGSL 
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NAME/KEY: SITE
LOCATION: (234)
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US-09-923-779-152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 GGSLISEDWVVTAAHCGVRTS-DVVVAGEFDQGSDEENIQVLKIAKVFKNPKFSILTVNN 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 DVTLLKLASPAQYTTRISPVCLASSNEALTEGLTCVTTGWGRLSGVGNVTPAHLQQVALP 180
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Patent No. US2002008165941

GENERAL INFORMATION:

APPLICANT: Rosen et al.

FILLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

FILLE REPRENCE: PA105

CURRENT FILING DATE: 2001-08-10

PRIOR APPLICATION NUMBER: PCT/US00/05989

PRIOR APPLICATION NUMBER: 60/124,270

PRIOR FILING DATE: 1999-03-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 LVTVNQCRQYWDSSITDSMICAGGAGASSCQGDSGGPLVCQKGNTWVLIGI 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 56.1%; Score 684.5; DB 10; Best Local Similarity 55.0%; Pred. No. 1.4e-54; Matches 127; Conservative 36; Mismatches 67;
                                                                                      APPLICANT: WHYTE, DAVID
APPLICANT: CARKEPEEL, SEAN
APPLICANT: CHARVEDCAK, GLEN
APPLICANT: MANNING, GERARD
APPLICANT: SUDARSANAM, SUCHA
TITLE OF INVENTION: NOVEL PROTEASES
FILE REFERENCE: 038602/1214
CURRENT APPLICATION NUMBER: US/09/88,615
CURRENT FILING DATE: 2001-06-26
PRIOR APPLICATION NUMBER: 60/214,047
PRIOR FILING DATE: 2000-06-26
NUMBER OF SEQ ID NOS: 150
SOFTWARE: PALENTIN VEY. 2.1
                 Sequence 96, Application US/09888615
Patent No. US20020064856A1
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SOFTWARE: PatentIn Ver. 2.0
                                                                          APPLICANT: PLOWMAN, GREGORY
                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Homo sapiens US-09-888-615-96
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ORGANISM: Homo sapiens
                                                      GENERAL INFORMATION:
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US-09-925-297-576
US-09-888-615-96
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LENGTH: 263
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LENGTH: 269
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                          NAME/KEY: SITE
LOCATION: (213)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (220)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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Xaa equals any of the naturally occurring L-amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59 FCGGSLISQSWVVTAAHCNVSPGRHFVVLGEYDRSSNAEPLQVLSVSRAITHPSWNSTTM 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 MIXTLLLSTLVAG-ALSCGDPTYPP---YVTRVVGGEBARPNSWPWQVSLQYSSNGKWYH
                                                                                                                                                                                                                                                                                                                                                                                               13;
                                                                                                                                                                                                                                                                                                                                     35.0%; Score 427.5; DB 10; Length 269;
43.9%; Pred. No. 2.1e-31;
Live 26; Mismatches 89; Indels 13;
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Batent No. US20020076721A1

GENERAL INFORMATION:

APPLICANT: Pyle, Kuth A.

APPLICANT: Pyle, Kalos, Michael D.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER FILE REFERENCE: 210121.553

CURRENT APPLICATION NUMBER: US/09/923,779

CURRENT FILING DATE: 2001-08-06

NUMBER OF SEQ ID NOS: 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       177 VALPLVIVNQCRQ--YWDSSITDSMICAGGAGA-SSCQGDSGGPLVCQ 221
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Best Local Similarity 43.9%
Matches 100; Conservative
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Best Local Similarity 40.78
Matches 98; Conservative
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Wei-Qiang
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                                                                                               ORGANISM: Homo sapiens
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                                                                                                                                               Query Match
Best Local Similarity
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US-09-978-295A-69
                                              SEQ ID NO 2
LENGTH: 343
                                                                                                                US-09-948-094-2
                                                                                TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: SITE
LOCATION: (28)
COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: SITE
LOCATION: (34)
COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-925-97-695
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Patent No. US20020090625A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: The Brigham and Women's Hospital, Inc.
APPLICANT: Work, Samuel
APPLICANT: Wong, Kwong-kwok
TITLE OF INVENTION: Methods of Detecting Cancer Based on Prostasin
FILE REFERENCE: 81994/282423
                                                                                                             Sequence 695, Application US/09925297
Patent No. US20020081659A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA105
                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/925,297
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/USO0/05989
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 1999-03-12
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 928
SOFTWARE: PATENTIN VET: 2.0
LENGTH: 273
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Best Local Similarity 40.7'
Matches 98; Conservative
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NAME/KEY: SITE
LOCATION: (27)
                                                                                RESULT 5
US-09-925-297-695
231 I 231
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic ITLE OF INVENTION: Acids Encoding the Same
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                                                                                                                                                                                                                                                                                                                                                                                          SWNSTTMNNDVTLLKLASPAQYTTRISPVCLASSNEALTEGLTCVTTGWGRLS-GVGNVT 170
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                                                                                                                                                                                                         Length 343;
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Pred. No. 9.8e-30;
                                                                                                                                                                                                                                              38; Mismatches
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CURRENT FILING DATE: 2001-10-15
CURRENT APPLICATION NUMBER: US/09/948,094
CURRENT FILING DATE: 2001-09-07
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PATENTIN VERSION 3.0
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Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
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Wood, William I.
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36.3%;
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Tumas, Daniel
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Roy, Margaret Ann
Shelton, David L.
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Fong, Sherman
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Kuo, Sophia S.
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PRIOR APPLICATION NUMBER: 60/08129
PRIOR FILING DATE: 1998-04-09
PRIOR FILING DATE: 1998-04-15
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PRIOR PRICATION NUMBER: 60/08138
PRIOR PRILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/08268
PRIOR APPLICATION NUMBER: 60/08268
PRIOR PRILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/08269
PRIOR PRILING DATE: 1998-04-22
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TITLE OF INVENTION: Acids Encoding the Same Fills Breezenge. Principle of Comment Principle of Comment Principle of Comment Principle of Comment Principle of Comment Principle of Comment Principle of Comment Principle of Comment Principle of Comment Principle of Comment Principle of Comment Principle of Comment Principle of Comment Principle of Comment Principle of Comment Principle of Comment Principle of Comment Principle of Comment Principle of Comment Principle of Comment Principle of Comment Principle of Comment Principle of Comment Principle of Comment Principle of Comment Principle of Comment Principle of Comment Principle of Comment Principle of Comment Principle of Comment Principle of Comment Principle of Comment Principle of Comment Principle of Comment Principle of Comment Principle of Comment Principle of Comment Principle of Comment Principle of Comment Principle of Comment Principle of Comment Principle of Comment Principle of Comment Principle of Comment Principle of Comment Principle of Comment Principle of Comment Principle of Comment Principle of Comment Principle of Comment Principle of Comment Principle of Comment Principle of Comment Principle of Comment Principle of Comment Principle of Comment Principle of Comment Principle of Comment Principle of Comment Principle of Comment Principle of Comment Principle of Comment Principle of Comment Principle of Comment Principle of Comment Principle of Comment Principle of Comment Principle of Comment Principle of Comment Principle of Comment Principle of Comment Principle of Comment Principle of Comment Principle of Comment Principle of Comment Principle of Comment Principle of Comment Principle of Comment Principle of Comment Principle of Comment Principle of Comment Principle of Comment Principle of Comment Principle of Comment Principle of Comment Principle of Comment Principle of Comment Principle of Comment Principle of Comment Principle of Comment Principle of Comment Principle of Comment Principle of Comment Principle of Comment Principle o
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APPLICATION NUMBER: 60/081049
FILING DATE: 1998-04-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       330 ENFPDGKVCWTSGWGATEDGGDASPV-LNHAAVPLISNKICNHRDVYGGIISPSMLCAGY 388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     213 YSSRIVGGNMSLLSQWPWQASLQ-FQGYHLCGGSVITPLWIITAAHCVYDLYLPKSWTIQ 271
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Best Local Similarity 39.9%; Pred. No. 2.1e-29;
Matches 83; Conservative 31; Mismatches 83
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PRIOR APPLICATION NUMBER: 60/085700
PRIOR APPLICATION NUMBER: 60/085700
PRIOR PILING DATE: 1998-05-15
PRIOR FILING DATE: 1998-05-15
PRIOR FILING DATE: 1998-05-15
PRIOR FILING DATE: 1998-05-15
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PRIOR APPLICATION NUMBER: 60/085580
PRIOR PILING DATE: 1998-05-15
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Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
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US-09-978-697-69
Sequence 69, Application US/09978697
Patent No. US:0020169284A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
                                                                                                                                           LICATION NUMBER: 60/085323
                                                                                                                                                                                         APPLICATION NUMBER: 60/085582
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Williams, P. Mickey
Wood, William I.
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Shelton, David L.
Stewart, Timothy A.
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Filvaroff, Ellen
Fong, Sherman
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Gerber, Hanspeter
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Kuo, Sophia S.
Napier, Mary A.
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Eaton, Dan
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Goddwski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
                                                                                        PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085323
PRIOR APPLICATION NUMBER: 60/085323
PRIOR APPLICATION NUMBER: 60/085592
PRIOR APPLICATION NUMBER: 60/085700
PRIOR PILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/08569
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/08559
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; Sequence 69, Application US/09978192A
; Patent No. US20020177553A1
APPLICATION NUMBER: 60/084643
                                      APPLICATION NUMBER: 60/085339
FILING DATE: 1998-05-13
                                                                              PRIOR APPLICATION NUMBER: 60/085338
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Gerritsen, Mary E.
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Roy, Margaret Ann
Shelton, David L.
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Filvaroff, Ellen
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Kuo, Sophia S.
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Best Local Similarity 39.99
Matches 83; Conservative
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Desnoyers, Luc
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Gao, Wei-Qiang
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APPLICANT: Ashkenazi, Avi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Baker Kevin P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eaton, Dan
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APPLICATION NUMBER: 60/081049 FILING DATE: 1998-04-08

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R APPLICATION NUMBER: 60/081071

R FILING DATE: 1998-04-08

R APPLICATION NUMBER: 60/081195

R FILING DATE: 1998-04-08

R APPLICATION NUMBER: 60/081203

R FILING DATE: 1998-04-09

R FILING DATE: 1998-04-09

R FILING DATE: 1998-04-15

R APPLICATION NUMBER: 60/081819

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R APPLICATION NUMBER: 60/081819

R FILING DATE: 1998-04-15

R APPLICATION NUMBER: 60/08188

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R FILING DATE: 1998-04-21

R APPLICATION NUMBER: 60/082568

R FILING DATE: 1998-04-21
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R FILING DATE: 1998-04-22
R FILING DATE: 1998-04-22
R APPLICATION NUMBER: 60/082604
R FILING DATE: 1998-04-22
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R FILING DATE: 1998-04-22
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R PILING DATE: 1998-04-23
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R APPLICATION NUMBER: 60/083554
R FILING DATE: 1998-04-29
R APPLICATION NUMBER: 60/083554
R FILING DATE: 1998-04-29
                                        APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVEWION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVEWION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVEWION: Acids Encoding the Same
FILE REFERENCE: P2630P1C9
CURRENT APPLICATION NUMBER: US/09/978,192A
CURRENT FILING DATE: 2001-07-30
PRIOR FILING DATE: 2001-07-30
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/06226
PRIOR FILING DATE: 1997-11-03
PRIOR FILING DATE: 1997-11-13
PRIOR FILING DATE: 1997-11-21
PRIOR FILING DATE: 1997-11-21
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/07763
PRIOR APPLICATION NUMBER: 60/07763
PRIOR FILING DATE: 1998-03-10
PRIOR FILING DATE: 1998-03-11
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R FILING DATE: 1998-03-20

R FILING DATE: 1998-03-20

R FILING DATE: 1998-03-20

R FILING DATE: 1998-03-25

R APPLICATION NUMBER: 60,079664

R FILING DATE: 1998-03-27

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APPLICATION NUMBER: 60/078910
FILING DATE: 1998-03-20
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APPLICATION NUMBER: 60/077791
FILING DATE: 1998-03-12
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FILING DATE: 1998-03-20
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FILING DATE: 1998-03-13
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FILING DATE: 1998-03-30
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FILING DATE: 1998-03-31
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FILING DATE: 1998-04-01
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Stewart, Timothy A. Tumas, Daniel
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APPLICATION NUMBER: 60/083559 FILING DATE: 1998-04-29 APPLICATION NUMBER: 60/083500 APPLICATION NUMBER: 60/083742

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APPLICATION NUMBER: 60/08441 FILING DATE: 1998-05-06 APPLICATION NUMBER: 60/084637 FILING DATE: 1998-05-07

APPLICATION NUMBER: 60/084640 FILING DATE: 1998-05-07 APPLICATION NUMBER: 60/084598 ILING DATE: 1998-05-07

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PRICE APPLICATION NUMBER: 60/063120
PRICE FILING DATE: 1997-10-17
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PRICE PLING DATE: 1997-10-24
PRICE PLING DATE: 1997-10-28
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PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082569
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33.5%; Score 408.5; 39.9%; Pred. No. 2.10
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                                                   R FILING DATE: 1998-05-07

R APPLICATION NUMBER: 60/084627

R RAPLICATION NUMBER: 60/084643

R APPLICATION NUMBER: 60/085339

R FILING DATE: 1998-05-07

R RAPLICATION NUMBER: 60/085339

R FILING DATE: 1998-05-13

R RFILING DATE: 1998-05-13

R RPLICATION NUMBER: 60/085338

R FILING DATE: 1998-05-13

R RFILING DATE: 1998-05-13

R RPLICATION NUMBER: 60/085582
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R APPLICATION NUMBER: 60/085700

RR FILING DATE: 1998-05-15

R APPLICATION NUMBER: 60/08569

RR FILING DATE: 1998-05-15

R APPLICATION NUMBER: 60/085579

R FILING DATE: 1998-05-15

R APPLICATION NUMBER: 60/085580

R FILING DATE: 1998-05-15

R APPLICATION NUMBER: 60/085580
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APPLICATION NUMBER: 60/085704
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DATE: 1998-05-07
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Watanabe, Colin K.
Wood, William I.
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Godowski, Paul
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Matches 83; Conserv
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PRIOR APPLICATION NUMBER: 60/08120
PRIOR FILING DARE: 1998 -04-22
PRIOR APPLICATION NUMBER: 60/08132
PRIOR PELLING DARE: 1998 -04-29
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PRIOR PELLING DARE: 1998 -05-07
PRIOR PELLING DARE: 1998 -05-15
PRIOR APPLICATION NUMBER: 60/08579
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PRIOR PELLING DARE: 1998 -05-15
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PRIOR PELLING DARE: 1998 -05-16
PRIOR PELLING DARE: 1998 -05-17
PRIOR PELLING DARE: 1998 -05-17
PRIOR PELLING DARE: 1998 -05-17
PRIOR PELLING DARE: 1998 -06-07
PRIOR PELLING DARE: 19
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TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA106
CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
SOFTWARE: PatentIN Ver. 2.0
SEQ ID NO 1017
LENGTH: 248
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RR FILING DATE: 1998-06-16
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PR FILING DATE: 1998-06-17

PR APPLICATION NUMBER: 60/089598

PR FILING DATE: 1998-06-17

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PR FILING DATE: 1998-06-17
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Best Local Similarity 39.9%
Matches 83; Conservative
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87 LGEYDRSSNAEPLQVLSVSRAITHPSWNSTTMNNDVTLLKLASPAQYTTRISPVCLASSN 146
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ilarity 40.2%; Pred. No. 1.5e-29;
Conservative 31; Mismatches 82;
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40.2%; Pred. No. 2.3e-29;
tive 31; Mismatches 82;
CURRENT PERIORICATION NUMBER: US/09/946,633
CURRENT FILING DATE: 2001-09-06
PRIOR FILING DATE: 2001-09-06
PRIOR FILING DATE: 2000-06-20
PRIOR FILING DATE: 1999-06-20
PRIOR PELING DATE: 1999-05-07
PRIOR PELING DATE: 1999-05-07
PRIOR PELING DATE: 1999-06-20
PRIOR PELING DATE: 1999-06-20
PRIOR PELING DATE: 1999-06-20
PRIOR FILING DATE: 1999-06-30
PRIOR FILING DATE: 1999-09-09
PRIOR FILING DATE: 1999-09-09
PRIOR FILING DATE: 1999-09-09
PRIOR FILING DATE: 1999-11-01
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PATENTIN VET: 2.0
SSOFTWARE: 327
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Fatent No. US20020064856A1
GENERAL INFORMATION:
APPLICANT: PLOWMAN, GREGORY
APPLICANT: WHYTE, DAVID
APPLICANT: CARINDEEL, SEAN
APPLICANT: CARINDEEL, SEAN
APPLICANT: CARRING, GERARD
APPLICANT: SUDARSANAM, SUCHA
FILE OF INVENTION: NOVEL PROTEASES
FILE REPERENCE: 038602/1214
CURRENT FILING DATE: 2001-06-26
PRIOR PILING DATE: 2001-06-26
PRIOR FILING DATE: 2001-06-26
PRIOR FILING DATE: 2001-06-26
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Best Local Similarity 40.2%
Matches 84; Conservative
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CORGANISM: Homo sapiens
US-09-888-615-103
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US-09-946-633-8
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Best Local Similarity
Matches 84; Conserv
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TITLE OF INFORMATION:
TITLE OF INFORMATION Serine protease Polynucleotides, Polypeptides, and Antibodies
TITLE OF INVERNION:
TITLE OF INVERNION:
TITLE OF INVERNION:
TITLE OF INVERNION SERINE PROSPA
CURRENT APPLICATION NUMBER: US/09/804,156
CURRENT FILING DATE: 2001-03-13
PRIOR FILING DATE: 2000-03-14
NUMBER OF SEQ ID NOS: 38
SSOFWARE: Patentin Ver. 2.0
SSOFWARE: Patentin Ver. 2.0
LENGTH: 327
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                                                                        Length 248;
                                                                                                                  Indels
                                                                     Query Match 33.4%; Score 408; DB 10; Best Local Similarity 40.2%; Pred. No. 1.1e-29; Matches 84; Conservative 31; Mismatches 82;
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Patent No. US20020119925A1
GENERAL INFORMATION:
APPLICANT: Ni et al.
TITLE OF INVENTION: PT005P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Homo sapiens
US-09-804-156-16
         ORGANISM: Homo sapiens
                           US-09-925-301-1017
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                                                                                                      132 QYTTRISPVCLASSNEALTEGLICVTTGWGRLSGVGNVTPAHLQQVALPLVTVNQCRQY- 190
                       147 EALTEGLICVITGWGRL-SGVGNVTPAHLQQVALPLVIVNQC--RQYWDSSITDSMICAG 203
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30 FSQRIVNGENAVLGSWPWQVSLQDSSGFHFCGGSLISQSWVVTAAHCNVS---PGRHFVV 86
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                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:

APPLICANT: Abbott Laboratories

APPLICANT: Henchin, Jack

APPLICANT: Henchin, Jack

APPLICANT: Henchin, Jack

APPLICANT: Henchin, Jack

APPLICANT: Henchin, Donald J.

TITLE OF INVENTION: ANTIANGIOGENIC POLYPEPTIDES AND METHODS

TITLE OF INVENTION: FOR INHIBITING ANGIOGENESIS

FILE REFERENCE: 6738 US. 02

CURRENT APPLICATION NUMBER: US/09/967,386

PRIOR APPLICATION NUMBER: US 60/236,550

PRIOR APPLICATION NUMBER: US 60/236,550

PRIOR APPLICATION NUMBER: US 60/236,550

PRIOR FILING DATE: 2000-09-29

NUMBER OF SEQ ID NOS: 7

SOFTWARE: FASTEED for Windows Version 4.0

LENGTH: 791
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                                                                                                                                                                                                                                          Sequence 1, Application US/09967386 Patent No. US20020159992A1
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ORGANISM: Homo sapiens
US-09-967-386-1
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1 MLLLSLTLSLVLLGSSWGCG........GDSGGPLVCQKGNTWVLIGI 231
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GenCore version 5.1.3
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Maximum Match 100%
Listing first 45 summaries
                                                                       OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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sp_bacteria:*
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_rodent:*
sp_virus:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*

sp_plant:*

sp_rvirus:* sp_bacteriap:* sp_archeap:*

## SUMMARIES

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	ΔI	29EQZ8	29D7P8	29ER05	39D960	29W7Q4	29W7Q3	29DC86	29CR35	29D8X8	29PWQ6	290052	292077	29D7T9	29W7P9	29DC82	29W7Q1
		11	11	11	11	13	13	11	11	11	13	11	13	11	13	11	13
	Juery Match Length DB	264	264	264	264	261	260	263	263	263	263	269	266	269	260	164	249
æ	Query Match	90.3	89.5	89.5	88.7	62.8	58.2	56.1	55.9	55.4	55.2	38.7	38.1	38.0	37.2	36.6	36.2
	Score	1102	1093	1093	1083	766.5	710.5	684.5	682.5	6.979	674.5	472.5	465.5	464.5	454.5	447	442
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Gaps

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Query Match 90.3%; Score 1102; DB 11; Length 264; Best Local Similarity 87.0%; Pred. No. 5.1e-92; Matches 201; Conservative 17; Mismatches 13; Indels 0.

434 35.5 269 4 4 2 423 34.6 270 13 4 420.5 34.4 270 13 4 420.5 34.4 270 13 4 420.5 34.4 270 13 4 417.5 34.2 266 13 4 400.5 32.8 257 6 0 400.5 32.8 257 6 0 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	Q96qv5 homo saplen Q9bk47 luidia foli Q91039 gadus morhu Q96q18 homo saplen Q96q18 homo saplen Q96899 scolopendra Q96899 scolopendra Q95kw7 bos taurus Q9w7q2 paralichthy Q9w7q2 paralichthy Q9lf4 mus musculu Q9144 mus musculu Q8gqf6 xenopus lae Q15146 homo saplen Q15146 homo saplen Q1546 homo saplen Q4508 petromyzon Q4508 petromyzon Q40dgr2 xenopus lae Q4260 petromyzon Q9dgr2 xenopus lae Q42184 mus musculu Q9v6d drosophila P79953 xenopus lae Q921n4 mus musculu Q9v6d drosophila P79953 mus musculu Q9v6d drosophila Q91x79 mus musculu Q9v6d drosophila Q91x79 mus musculu Q91x79 mus musculu			odate) update)	Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rattus.	., Kato M., Sakagamī J.,	3J databases. S1; ALSO KNOWN AS THE				500E CRC64;
17 434 35.5 269 18 423 34.6 267 20 420.5 34.4 270 22 417.5 34.2 270 23 417.5 34.2 269 24 417.5 34.2 269 25 417.5 34.2 269 26 400.5 32.8 33.9 28 413 33.7 1268 29 39.9 32.7 469 31.0 400.5 32.8 32.8 33.9 29 39.5 32.7 263 39 39.5 32.7 263 39 39.5 32.7 263 39 39.5 32.7 263 39 39.5 32.7 263 39 39.5 32.7 263 39 39.5 32.7 263 39 39.5 32.7 263 39 39.5 32.7 263 39 39.5 32.7 263 39 39.5 32.7 263 39 39.5 32.7 263 39 39.5 32.7 263 39 39.5 32.7 263 39 39.5 32.6 247 39 39.5 32.7 263 39 39.5 32.7 263 39 39.5 32.7 263 39 39.5 32.7 263 39 39.5 32.7 263 39 39.5 32.7 263 39 39.5 32.7 263 39 39.5 32.7 263 39 39.5 32.7 263 39 39.5 32.7 263 39 39.5 32.7 263 39 39.5 32.7 263 39 39.5 32.7 263 39 39.5 32.7 263 39 39.5 32.7 263 39 39.5 32.7 263 39 39.5 32.7 263 39 39.5 32.7 263 39 39.5 32.7 263 39 39.5 32.7 263 39 39.5 32.7 263 39 39.5 32.7 263 39 39.5 32.7 263 39 39.5 32.7 263 39 39.5 32.7 263 39 39.5 32.7 263 39 39.5 32.7 263 39 39.5 32.7 263 39 39.5 32.7 263 39 39.5 32.7 263 39 39.5 32.7 263 39 39.5 32.7 263 39 39.5 32.7 263 39 39.5 32.7 263 39 39.5 32.7 263 39 39.5 32.7 263 39 39.5 32.7 263 39 39.5 32.7 263 39 39.5 32.7 263 39 39.5 32.7 263 39 39.5 32.7 263 39 39.5 32.8 32.8 260 20	0960V5 09BK47 0960L03 0960L03 0960L03 0960L03 0960L03 0990L04 0990L04 0990L04 0990L04 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05 0990L05	ALIGNMENTS	RT; 264	Created) Last sequence update) Last annotation update)	a; Craniata; Vert a; Sciurognathi;	ka K., Kashima K.	n."; nBank/DDE E FAMILY	ř	rypsin. otease_Try. TN	NMC	ER; 1. W; F9ED5D210FD3500E CRC64;
m G	25.5 4.4.4.6.6 4.4.4.6.6 4.4.4.7.2 4.4.4.2 4.4.2.7 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4.7.2 4		PRELIMINARY;	(TrEMBLrel. 16, (TrEMBLrel. 16, (TrEMBLrel. 21,	egicus (Rat). Metazoa; Chordat Utheria; Rodenti 10116;	OM N.A. PANCREAS; Mitsui S., Katao	cloning of rat c DEC-1998) to the	FAMILY. 757; BAB20287.1; 6; 4CHA. .256;	PR001314; Chymot PR001254; Ser_pr 89; trypsin; 1, 0772; CHYMOTRYPS	020; Tryp_SPC; 1 50240; TRYPSIN_D 00134; TRYPSIN_H	Serine protease. 264 AA; 28116 M
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Mismatches

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Matches 198; Conservative
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X MEDLINE-21085660; PubMed=1121785;

X Rawal J., Shinagawa A., Shibata K., Yoshino M., Itch M., Ishii Y.,

X Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

Arakawa T., Hara A., Ribbata K., Yoshino H., Adachi J., Fukuda S.,

X Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Salto T., Okazaki T., Golobori T., Bono H., Kasukwa T., Salto R.,

K Adota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

K Rubhl P., Lewis S., Matsuo Y., Nikaido I., Kasukawa H.,

K Nehl P., Lewis S., Matsuo Y., Nikaido I., Rochiwa H.,

K Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Brownstein M.J., Buli C., Eletcher C., Fujita M., Gariboldi M.,

Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Lyons P., Marchiond L., Masshima J., Mancanelli R., Romanerts P.,

Nordone P., Ring B., Ringwald M., Rodiiguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Ruzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

W Hayashizaki Y.,

K Wanshawa Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Hayashizaki Y.,
                                                                                                                                                                                                                                 61 GGSLISQSWVVTAAHCNVSPGRHFVVLGEYDRSSNAEPLQVLSVSRAITHPSWNSTTMNN 120
                                                                                                                                                                                                    121 DVTLLKLASPAQYTTRISPVCLASSNEALTEGLTCVTTGWGRLSGVGNVTPAHLQQVALP 180
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                            1 MLLLSLTLSLVLLGSSWGCGIPAIKPALSFSQRIVNGENAVLGSWPWQVSLQDSSGFHFC
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-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Functional annotation of a full-length mouse cDNA collection.";
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                                                                                                                                                                                                                                                                                                                           181 LVTVNQCRQYWDSSITDSMICAGGAGASSCQGDSGGPLVCQKGNTWVLIGI
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Last annotation update)
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PRINTS: PR00722; CHYMOTRYPSIN.
SMART; SM00020; TTYP_SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_LHIS; UNKNOWN_1.
PROSITE; PS00135; TRYPSIN_ESR; 1.
Hydrolase; Serine protease.
SEQUENCE 264 AA; 28167 MW; 1D979469A070
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Best Local Similarity
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1 MLLLSLTLSLVLLGSSWGCGIPAIKPALSFSQRIVNGENAVLGSWPWQVSLQDSSGFHFC 60
                       1 MLLISLTLSLVLLGSSWGCGVPAITPALSYNQRIVNGENAVPGSWPWQVSLQDNTGPHFC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bjoernslett M.; Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
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                                                                                                                                                                                                                                                                                                                               181 LVTVNQCRQYWGARITDAMICAGGSGASSCQGDSGBPLVCQKGNTWVLIGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. Mitsul S., Yamaquchi N.; Mitsul S., Yamaquchi N.; "Molecular cloning of mouse chymopasin."; Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28135 MW; 1D979709A07056C2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 89.5%; Score 1093; DB 11;
Best Local Similarity 85.7%; Pred. No. 3.3e-91;
Matches 198; Conservative 21; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEROPS; 201.256; -..
MGD; MGI:88558; Ctrl.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
PRINTS; PR00702; CHYMOTRYPSIN.
PROSTE; PS50240; Tryp_SPC; 1.
PROSITE; PS00134; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_LER; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
PROFITE; PS00135; TRYPSIN_SER; 1.
PROFITE; PS00135; TRYPSIN_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2001 (TrEMBLrel. 16, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN=129S6/SVEVTAC; TISSUE=SPLEEN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chymopasin (Chymotrypsin A CTRA-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF236365; BAB20275.1; -. EMBL; AF236365; AAL11034.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2001 (TrEMBLrel. 16, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P00766; 4CHA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTRL OR CTRA1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121
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DVTLLKLASPAQYTTRISPVCLASSNEALTEGLTCVTTGWGRLSGVGNVTPAHLQQVALP 180
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                                                                                                                                                                           09W704;
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                                                                                                                                                          09W7Q4
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                 121
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Q9W7Q3
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09W7Q4
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                                                                                                                                                                                                                                                                                                  RA Kawai J. Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Rawai J., Shinagawa A., Fukuaishi Y., Konno H., Adachi J., Pukuda S., Alzawa M., Nishi K., Konno H., Adachi J., Pukuda S., RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Balalov S., Casavant T., RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Ouackenbush J., RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Ouackenbush J., RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Schrimi L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., RA Buthon D., Kamiya M., Lee N. H., A Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., RA Hassilzani Y., Kowaji H., Kohtsuki S.,
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GGSLISQSWVVTAAHCNVSPGRHFVVLGEYDRSSNAEPLQVLSVSRAITHPSWNSTTMNN 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 409:685-690(2001).
-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88.7%; Score 1083; DB 11; Length 264; 85.3%; Pred. No. 2.7e-90; 1.ve 21; Mismatches 13; Indels 0.
                                                     1D979719E07C16DE CRC64;
                                                                                                                                 Ol-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
18100040151k protein.
CTRL OR 1810004015RIK.
Mus musculus (Monico.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGD: MGI:8858; Ctrl.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001354; Ser_protease_Try.
Ffam: PF00089; trypsin: 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SWART; SW00020; Tryp_SPC: 1.
PROSITE; PS50240; TRYPSIN_DOW; 1.
PROSITE; PS00134; TRYPSIN_LS; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AK007333; BAB24967.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28151 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hydrolase; Serine protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 85.3 les 197; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP; P00766; 4CHA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           264 AA;
                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
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Matches
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                                                                                                       RESULT 4
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59 GGSLISPYWVVTAAHCTVSPRNHRVILGEHDRQYNNEDIQVMSIARAITHPYYNSQNFNN 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 DVTLLKLASPAQYTTRISPVCLASSNEALTEGLTCVTTGWGRLSGVGNVTPAHLQQVALP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          119 DITLLRLSSPVQMTSRVSPVCLASSSTSIPSGTKCVTTGWGRTGQTS--SPRYLQQTSLP 176
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                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Taleostei; Biteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
Pleuronectoidei; Paralichthyidae; Paralichthys.
Suzuki T., Srivastava A.S., Kurokawa T.; "Japanese flounder mRNA for chymotrypsinogen 1."; Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases. --- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MLLLSLTLSLTLGSSWGCGIPAIKPALSFSQRIVNGENAVLGSWPWQVSLQDSSGFHFC
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                                                                    231
                                                                                           Indels
                                                                    181 LVTVNQCRQYWDSSITDSMICAGGAGASSCQGDSGGPLVCQKGNTWVLIGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28184 MW; D7090A9D65395B7D CRC64;
                                                                                                                                                                                                                                                                                           01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 766.5; DB 13;
Pred. No. 1.3e-61;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; 1970.

InterPro; 198001254; Ser_protease_Try.
InterPro; 198001254; Ser_protease_Try.
Pfam; PF000089; trypabin; 1.
SMART; SM00020; Tryp_SPG: 1.
PROSITE; PS50240; TRYPSIN_DOW; 1.
PROSITE; PS00134; TRYPSIN_LSB; 1.
PROSITE; PS00135; TRYPSIN_LSB; 1.
PHYDrolase; Serine protease.
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                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                         Chymotrypsinogen 1.
Paralichthys olivaceus (Flounder).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AB029753; BAA82365.1; -. HSSP; P00763; 1DPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62.8%;
61.6%;
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                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   261 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID-8255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-PANCREAS;
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PRELIMINARY;
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                                                                                                                                                                                                                                                     MEROPS; S01.152;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70 VVTAAHCNVSPGRHFVVLGEYDRSSNAEPLQVLSVSRAITHPSWNSTTMNNDVTLLKLAS 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   130 PAQYTTRISPVCLASSNEALTEGLTCVTTGWGRLSGVGNVTPAHLQQVALPLVTVNQCRQ 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              126 PAQMNMRVSPVCVAETSDNFAGGMKCVTSGWGLTRHNAPDTPALLQQAALPLLTNDDCRR 185
                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 LVLLGSSWGCGIPAIKPALSFSQRIVNGENAVLGSWPWQVSLQDSSGFHFCGGSLISQSW 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=C57BL/G3; TISSUE=SPLEEN;
MEDLINE=21085660; PubMed=11217851;
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
                       Paralichthys Olivaceus (Flounder).

Bukaryota: Metazoa: Chordata: Craniata: Vertebrata: Buteleostomi;

Actinopterygii: Teleostei; Buteleostei; Neoteleostei;

Acanthomorpha: Acanthopterygii; Percomorpha: Pleuronectiformes;

Pleuronectoidei; Paralichthyidae; Paralichthys.
                                                                                                                                              Suzuki T., Srivastava A.S., Kurokawa T.;
Suzuki T., Srivastava A.S., Kurokawa T.;
Japanese flounder mRNA for chymotrpsinogen 2.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
-i- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
EMBL; AB029754; BAA82366.1; -.
HSSP; P00766; 1CHG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                      58.2%; Score 710.5; DB 13; Length 260; 57.7%; Pred. No. 1.6e-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                  57; Indels
                                                                                                                                                                                                                                                                              Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SWART; SW00702; CHYMOTRYPSIN.
PROSITE; PS00134; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_SER; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
HYDCOLASE; SETINE POTCHESE; 1.
SEQUENCE 260 AA; 27793 MW; 9F583044E22F78C0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       190.YWDSSITDSMICAGGAGASSCQGDSGGPLVCQKGNTWVLIGI 231
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                  36; Mismatches
                                                                                                                                                                                                                                        MEROPS; S01.152; --
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 128; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                      SEQUENCE FROM N.A.
TISSUE=PANCREAS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                           NCBI_TaxID=8255
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01-JUN-2002
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Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washlo T., Sakai K., Okido T., Frurno M., Anon H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gartiboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Salosuki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Winshelbert B., Kawaji H., Kohtsuki S.,
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"Functional annotation of a full-length mouse cDNA collection.";
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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STRAIN=C57BL/6J; TISSUE=STOMACH, SPLEEN, AND PANCREAS;
MEDLINE=21085660; PubMed=11217851;
Kawai J., Shinaqawa A., Shibata K., Yoshino M., Itoh M., Ishii
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda Arakawa T., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka
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Last annotation update)
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SMART; SMO0020; TRYP_SEP: 1.
PROSTIE; PS50240; TRYPSIN_DOM; 1.
PROSTIE; PS00134; TRYPSIN_LIS; UNKNOWN_1.
PROSTIE; PS00135; TRYPSIN_ERR; 1.
PROSTIES; SC110e protease; Serine protea
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InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00089; trypsin; 1.
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Query Match
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GGSLISQSWVVTAAHCNVSPGRHFVVLGEYDRSSNAEPLQVLSVSRAITHPSWNSTTMNN 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                            1 MILLSLTLSLVLLGSSWGCGIPAIKPALSFSQRIVNGENAVLGSWPWQVSLQDSSGFHFC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                       "Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-590(2001).
-1-SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
TRYPSIN FAMILY.
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                             Query Match 55.9%; Score 682.5; DB 11; Best Local Similarity 54.5%; Pred. No. 5.6e-54; Matches 126; Conservative 37; Mismatches 67;
                                                                                                                                                                                                                                                          InterPro: IPR001254; Chymotrypsin.
InterPro: IPR001254; Ser_protease_Try.
Pfam: PF000089; trypsin: 1.
PRINTS: PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM; IPROSITE; PS00134; TRYPSIN_LSE; 1.
PROSITE; PS00135; TRYPSIN_ER; 1.
Hydrolase; Serine protease.
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                                                                                                                                                                           EMBL, AK008927; BAB25971.1; --
BMBL, AK003079; BAB22553.1; --
EMBL, AK007765; BAB25241.1; --
EMBL, AK007815; BAB25280.1; --
EMBL, AK008789; BAB25861.1; --
EMBL, AK00888; BAB25861.1; --
EMBL, AK00888; BAB25954.1; --
HSSP; P00766; IGCT.
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MGD; MGI:1913723; 2200008D09R1k
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01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2002 (TrEMBLrel. 21,
2200008D09R1K, protein.
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                                                                                                                                                                                                                                                                                                                                              263 AA;
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                                                                                                                                Hayashizaki Y.;
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A STARING-STRING-STRING-PANCREAS;

STRAIN-CSTBL/GG; TISSUE-PANCREAS;

REDLINE-21085660; PubMed-11217851;

RAMAI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Arawa T., Hara A., Eukunishi Y., Konno H., Adachi J., Fukuda S.,

A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Saburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Saburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Suzuki R., Tomita M., Wagner L., Washio T.,

Sakin K., Okido T., Furuno M., Anno H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Ruonstein M.J., Bult C., Fletcher C., Fujita M., Manbaerts P.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Rordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Saxaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Nordone P., Ring B., Ringwald M., Weltz C., Whittaker C., Wilming L.,

Nordone P., Rons R., Wang K., Wang K.H., Wettz C., Whittaker C., Wilming L.,

Nordone P., Rons R., Wang K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Nordone P., Rons R., Wang K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 409:685-690(2001).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Functional annotation of a full-length mouse cDNA collection.";
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SMART; SM00020; TYP_SPC; 1.
PROSITE; PSC0240; TRYPSIN_DOM; 1.
PROSITE; PSC0134; TRYPSIN_HIS; UNKNOWN_1.
PROSITE; PSC0135; TRYPSIN_ESR; 1.
Hydrolase; Serine protease
SEQUENCE 263 AA; 27898 MW; C0638FBBF905A92F CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Chymotrypsin B precursor (EC 3.4.21.1).
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InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
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HSSP; P00766; 1GCT.
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Matches 125; Conservative
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Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
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MGD; MGI:1915118; Ela3b.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00089; trypsin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                        31;
                                                                                                                                                                         EMBL; AK010149; BAB26734.1; -. EMBL; AK009129; BAB26092.1; -. HSSP; P05805; 1FON.
                                                                                                                                                                                                                                                                                                                                                               38.7%;
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SEOUENCE 269 AA; 28904 N
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Best Local Similarity
  Schriml L.M.,
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                      73 AAHCNVSPGRHFVVLGEYDRS-SNAEPLQVLSVSRAITHPSWNSTTMNNDVTLLKLASPA 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     132 QYTTRISPVCLASSNEALTEGLTCVTTGWG--RLSGVGNVTPAHLQQVALPLVTVNQCRQ 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                        Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
                                                                  MEDLINE=20464334; PubMed=11011764;
Spilliaert R., Gudmundsdottir A.;
Molecular Cloning of the Atlantic Cod Chymotrypsinogen B.";
Microb. Comp. Genomics 5:41-50(2000).

-i- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chordata; Craniata; Vertebrata; Euteleostomi;
Rodentia; Sciurognathi; Muridae; Mus
                                                                                                                                                                                                                                                                                                                             Length 263;
            Acanthomorpha; Paracanthopteryqii; Gadiformes; Gadidae; Gadus
                                                                                                                                                                                                                                                                                                                                                   51; Indels
                                                                                                                                                                                                                                                                                                      EF61B18A34EE5E7C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              190 YW-DSSITDSMICAGGAGASSCQGDSGGPLVCQKGNTWVLIGI 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                            55.2%; Score 674.5; DB 13; 57.0%; Pred. No. 3e-53;
                                                                                                                                                                                   CHYMOTRYPSIN B.
                                                                                                                                                                                                                                                                                                                                                   38; Mismatches
                                                                                                                                                                     InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
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01-JUN-2001 (TrEMBLrel. 17, Last sequ
01-JUN-2002 (TrEMBLrel. 21, Last anno
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MEDLINE=21085660; PubMed=11217851;
                                                                                                                                      EMBL; AJ242521; CAB43766.1; -. HSSP; P00766; 1CHG.
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01-JUN-2002 (TrEMBLrel.
2310074F01Rik protein.
ELA3B OR 2310074F01RIK.
                                                          IISSUE-PYLORIC CAECA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                      263 AA;
                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                              MEROPS; S01.152; -
                                              SEQUENCE FROM N.A.
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Sakai K., Okido T., Furuno M., Anno H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bolunga N., Carninci P., de Bonaldo M.P., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustinoich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchlonni L., Maschima D., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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MEDLINE-96562679; PubMed-8925447;
Gudmundsdottir E., Spilliaert R., Yang Q., Craik C.S., Bjarnason J.B.,
Gudmundsdottir A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57 CGGSLITPDWVLTAGHCISTSRTYQVVLGEHERGVEEGQEQVIPINAGDLFVHPKWNSMC 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      116 TTMNNDVTLLKLASPAQYTTRISPVCLASSNEALTEGLTCVTTGWGRLSGVGNVTPAHLQ 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15; Gaps
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Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Gadus.
NCBI_TaxID=8049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 LLSLTLSLVLLGSSWGCGIPAIKPALSFSQRIVNGENAVLGSWPWQVSLQ---DSSGFHF
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01-NOV-1996 (TTEMBLrel. 01, Last sequence update)
01-UON-2002 (TTEMBLrel. 21, Last annotation update)
Elastase precursor (EC 3.4.21.37) (Leukocyte elastase) (Lysosomal elastase) (Neutrophil elastase) (Bone marrow serine protease)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                               "Functional annotation of a full-length mouse cDNA collection."; Nature 409:682-590(2001).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
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Pred. No. 6.3e-35;
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SMART; SMOD020; Tryp_SPc; 1.
SMART; PS50240, TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
PROSITE; PS00135; TRYPSIN_HIS; UNKNOWN_1.
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PRT;
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HSSP; P05805; 1FON.
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MEDLINE—21085660; PubMed=11217851;
MEDLINE—21085660; PubMed=11217851;
MEDLINE—21085660; PubMed=11217851;
MEDLINE—21085660; PubMed=11217851;
MEDLINE—21085660; PubMed=11217851;
Marawa T., Shibara K., Kiyosawa H., Rondo S., Yamanaka I.,
Arawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Salto T., Okazaki Y., Golobori T., Bono H., Kasukawa T., Saito R.,
Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,
Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MKLLVFALFVAGAYGCGLPTFPPIVT---RVVGGEDVRVHSWPWQASLQYKSGNSFYHTC 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
E13100746701R1K.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                      encoding two distinct psychrophilic elastases.";
Comp. Biochem. Physiol. 113B:795-801(1996).
-!- CATALYTIC ACTIVITY: HVDROLYSIS OF PROTEINS, INCLUDING ELASTIN.
-!- SIMILARITY: BELONGE: VAL-!-XAA > ALA-!-XAA.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PLVTVNQCRQY - - WDSSITDSMICAGGAGA - SSCQGDSGGPLVCQKGN - TWVLIGI 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Isolation and characterization of two cDNAs from Atlantic cod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27 ACTIVATION PEPTIDE (POTENTIAL).
266 ELASTASE.
28533 MW. B786B52C71559E2E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Score 465.5; DB 1;
; Pred. No. 2.7e-34;
45; Mismatches 83.
                                                                                                                                                                                                                                                                           PRINTS, PRO0089; trypsin; I.
PRINTS, PR00722; CHYMOTRYPSIN.
SMART; SM00020; TrypSSPC; I.
PROSITE; PS50240; TRYPSIN.DOM; I.
PROSITE; PS00134; TRYPSIN.HIS; UNKNOWN_I.
PROSITE; PS00135; TRYPSIN.ERF; I.
PROSITE; PS00135; TRYPSIN.SER; I.
ISSUIGNAL.
                                                                                                                                                                                                   MEROPS, S01.155; -.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
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40.3%;
                                                                                                                                                                 EMBL; U56956; AAB58350.1; -. HSSP; P05805; 1FON.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
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Lyons P., Marchionni L., Mashima J., Mazzarelli J., Monbaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Satto K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   116 TIMNNDVTLIKLASPAQYTTRISPVCLASSNEALTEGLICVTTGWGRLSGVGNVTPAHLQ 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           176 QALLPVVDYEHCSRWNWWGLSVKTTMVCAGGDIQSGCNGDSGGPLNCPADNGTWQVHGV 234
Kamiya M., Lee N.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NAR-2002 (TrEMBLrel. 20, Last annotation update)
Elastase 4 (Fragment).
Paralichthys olivaceus (Flounder).
Paralichthys olivaceus (Flounder).
Actinopterygii, Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthomorpha; Acanthomorpha; Paralichthydiae; Paralichthydiae; Paralichthydiae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Suzuki T., Srivastava A.S., Kurokawa T.;
Japanese E flounder mRNA for elastasse 4 precursor.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
EMBL; AB039758; BAA82370.1; -.
HSSP; P00761; 1EPT.
                                                                                                                                                                                                                                      Nature 409:685-690(2001).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection.";
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InterPro; IPR001314; Chymotrypsin.
InterPro; IPR00124; Ser_protease_Try.
Pfan: PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SMO020; Tryp_SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_DOM; 1.
PROSITE; PS00135; TRYPSIN_LSER; 1.
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RAWAI J. Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RAWAI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arawawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Arawawa T., Hara A., Fukunishi Y., Konno H., Kasukawa T., Zamanaka I.,
RA Aizawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Aizawa K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Achriml L.M., Staubli F., Joshia B., Kochiwa H.,
Rochiml L.M., Staubli F., Zuzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Blake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoebach C., Seya T., Shibata Y., Storch K.-F.,
Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
Narachiani, V.,
                                                                                                                                                                                                                                                                                                                                             65 ISQSWVVTAAHCNVSPGRHFVVLGEYDRSSNAEPLQVLSVSRAITHPSWNSTTMNNDVTL 124
                                                                                                                                                                                                                                                                                                                                                                                              125 LKLASPAQYTTRISPVCLASSNEALTEGLTCVTTGWGRLSGVGNVTPAHLQQVALPLVTV 184
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                                                                                                                                                                                                                                                                            LSLVLLGSSWGCGIPAIKPALSFSQRIVNGENAVLGSWPWQVSLQDSSG---FHFCGGSL 64
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                        13;
                                                                                                                                                                                         DB 13; Length 260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   185 NQCRQ--YWDSSITDSMICAGGAG-ASSCQGDSGGPLVCQK-GNTWVLIGI 231
                                                                                                                                                                                       ; Score 454.5; DB 13; Length
; Pred. No. 2.6e-33;
45; Mismatches 80; Indels
                                                                                                                                                       260 AA; 27942 MW; 61883CD1B6A66075 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
               Pfam; PF00089; trypsin; I.
PRINTS; PR00722; CHYMOTRYPPIN.
SMART; SMO0020; Tryp_SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_LHIS; UNKNOWN_I.
PROSITE; PS00135; TRYPSIN_SER; 1.
Hydrolase; Serine protease.
NON_TER 1 1
SEQUENCE 260 AA; 27942 MW; 61883CD1B6A6
InterPro; IPR001254; Ser_protease_Try.
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01-JUN-2002 (TTEMBLTE1. 21,
0910001G08Rik protein.
CTRL OR 0910001G08RIK.
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EMBL; AK003074; BAB22549.1;
HSSP; P00763; 1DPO.
                                                                                                                                                                                         37.2%;
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                                                                                                                                                                                                                          93; Conservative
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                                                                                                                                                                                                          Best Local Similarity
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                                                                                                                                                                                       Query Match
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Q9DC82;
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Q9DC82
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110 HPSWNST-TMNNDVTLLKLASP-AQYTTRISPVCLASSNEALTEGLTCVTTGWGRLSGVG 167
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                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                               5
                                                                                                                                                                      Length 164;
                                                                                                                                17707 MW; 83791FD829ABEDD6 CRC64;
                                                                                                                                                                      Score 447; DB 11
Pred. No. 7e-33;
                                                                                                                                                                                                                 9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search completed: December 20, 2002, 15:18:53 Job time: 29.6087 secs
InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00089; trypsin; 1.
SMART: SM00020; Tryp_SPc; 1.
PROSITE; PS550240; TRYPSIN_DOM; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
Hydrolase; Serine protease.
SEQUENCE 164 AA; 17707 MW; 8379IFD82
                                                                                                                                                                      7 Match 36.6%;
Local Similarity 69.4%;
nes 86; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          228 LIGI 231
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                                                                                                                                                                          Query Match
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ALIGNMENTS

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002844 P06871 P06871 P00762 P00762 P97435 P97435 P980627 P980628 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P980629 P9806

TRY3_SALSA
MCT7_MOUSE
TRY1_RAT
TRY1_RAT
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TRY1_RAT
TRY1_COUSE
TRY1_CHICK
TRY2_CHICK
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1210.790 Million cell updates/sec
                                                                 December 20, 2002, 15:12:58; Search time 7.91304 Seconds
                                                                                                       US-09-856-319B-2_COPY_1_231
1221
1 MLLLSLTLSLVLLGSSWGCG......GDSGGPLVCQKGNTWVLIGI
         GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd
                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                           112892 segs, 41476328 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Perfect score:
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Description		m	gadu		ratt	P00767 bos taurus	P80646 gadus morhu	P00766 bos taurus	sns		pos	P08217 homo sapien		рошо	homod	mus m	P05805 bos taurus	рошо	P57727 homo sapien	ratto	P81286 ovis aries	rattu		mus n	P12545 macaca mula	P98072 bos taurus	Q28153 bos taurus	s sns	Q99895 homo sapien	mus m	80010		Q05319 drosophila
ID	CTRL_HUMAN	CTR2_CANFA	CTRA_GADMO	CTRB_HUMAN	CTRB_RAT	CTRB_BOVIN	CTRB_GADMO	CTRA_BOVIN	EL2_PIG	EL3B_HUMAN	EL2_BOVIN	EL2A_HUMAN	EL2_RAT	EL2B_HUMAN	EL3A_HUMAN	EL2_MOUSE	CAC3_BOVIN	PSS8_HUMAN	TMS3_HUMAN	CLCR_RAT	PLMN_SHEEP	PSS8_RAT	PLMN_HUMAN	PSS8_MOUSE	PLMN_MACMU	ENTK_BOVIN	EL1_BOVIN	PLMN_PIG	CLCR_HUMAN	PLMN_MOUSE	- 1	TRYT_MERUN	STUB_DROME
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.

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or send an email to license@isb-sib.ch).
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CATALYTIC ACTIVITY: Preferential cleavage: Tyr-|-Xaa, Trp-|-Xaa, Phe-|-Xaa, Leu-|-Xaa.
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MEDLINE-84170253; PubMed-6584866;
Pinsky S.D., Laforge K.S., Luc V., Scheele G.;
Tidentification of cDNA clones encoding secretory isoenzyme forms: sequence determination of canine pancreatic prechymotrypsinogen 2 mRNA.";
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                    3F629F02FA6DDFB4 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHYMOTRYPSINGGEN 2.
                                             Score 1214; Db 1, No. 6.8e-98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SUBCELLULAR LOCATION: Extracellular.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-AUG-1987 (Rel. 05, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Chymotrypsinogen 2 precursor (EC 3.4.21.1).
Canis familiaris (Dog).
                                                                                                        0; Mismatches
BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SFC; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
                  28002 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-AUG-1987 (Rel. 05, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; K01173; AAA30841.1; -. PIR; A21195; A21195.
                                                               99.4%;
                                                                                                          Matches 230; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P00766; 1ACB. MEROPS; S01.152; -.
                    264 AA;
                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTR2_CANFA P04813;
DISULFID
                    SEQUENCE
                                                                 Query Match
                                                                                      Local
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                                                                                                                                                                                                                                                                                                                                                                  1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DVTLLKLASPAQYTTRISPVCLASSNEALTEGLTCVTTGWGRLSGVGNVTPAHLQQVALP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGSLISQSWVVTAAHCNVSPGRHFVVLGEYDRSSNAEPLQVLSVSRAITHPSWNSTTMNN 120
                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Pyloric caeca;
MEDLINE-9211252; PubMed-1764912;
MEDLINE-9211252; PubMed-1764912;
ASSGLINE-9211252; PubMed-1764912;
"Structural and kinetic properties of chymotrypsin from Atlantic cod (Gadus morhua). Comparison with bowine chymotrypsin.";
Comp. Blochem. Physiol. 998:337-335(1991).
-: CATALYTIC ACTIVITY: Preferential cleavage: Tyr-|-Xaa, Trp-|-Xaa,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MAFLWLLSCFALLGTAFGCGVPAIQPVLSGLSRIVNGEDAVPGSWPWQVSLQDSTGFHFC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Euteleostei; Neoteleostei;
                                                                                                                                                                                                                                                                                                                                                                                                                    1 MLLLSLTLSLVLLGSSWGCGIPAIKPALSFSQRIVNGENAVLGSWPWQVSLQDSSGFHFC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gadus morhua (Atlantic cod).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                  1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Atlantic cod cDNA encoding a psychrophilic chymotrypsinogen.";
Biochim. Biophys. Acta 1219:211-214(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleos
Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Gadus.
                                                                                                                                                                                                                                                                                                                    Length 263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 LVTVNQCRQYWDSSITDSMICAGGAGASSCQGDSGGPLVCQKGNTWVLIGI 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gudmundsdottir A., Oskarsson S., Eakin A.E., Craik C.S.,
CHYMOTRYPSIN 2, B CHAIN.
CHYMOTRYPSIN 2, C CHAIN.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                  2A2F449D813B3961 CRC64;
                                                                                                                                                                                                                                                                                                                                                                  64;
                                                                                                                                                                                                                                                                                                                  DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Phe-|-Xaa, Leu-|-Xaa.
-!- SUBCELLULAR LOCATION: Extracellular.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.
                                                                                                                                                                                                                                                                                                               58.5%; Score 714.5; DB 1
56.7%; Pred. No. 9.7e-55;
1ve 35; Mismatches 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-LUN-2002 (Rel. 41, Last annotation update)
Chymotrypsin A precursor (EC 3.4.21.1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Pyloric caeca;
MEDLINE=94368860; PubMed=8086467;
                                                                                                                                                                                                                                                               27787 MW;
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                                                                                                                                                                                                                                                                                                                  Query Match 58.5%
Best Local Similarity 56.7%
Matches 131; Conservative
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       164
263
75
75
120
213
76
219
200
238
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167
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154
186
209
263 AA;
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RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                              132 QYTTRISPVCLASSNEALTEGLICVTTGWGRLSGVGNVTPAHLQQVALPLVTVNQCRQYW 191
                                                                                                                                                                                                                                                                                                                                                                                       72 TAAHCNVSPGRHFVVLGEYDRSSNAEPLQVLSVSRAITHPSWNSTTMNNDVTLLKLASPA 131
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                                                                                                                                                          SIMILARITY).
SIMILARITY).
SIMILARITY).
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Sukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID-9606;
                                            InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR00125; CHYMONTRYPSIN.
SMART; SM00020; Tryp_SPC; 1.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS00134; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_ERE; 1.
PROSITE; PS00135; TRYPSIN_ERE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Pancreas;
MEDLINE-89134264; PubMed-2917002;
Tomita N., Izumoto Y., Horii A., Doi S., Yokouchi H., Ogawa M.,
Mori T., Matsubara K.;
"Molecular cloning and nucleotide sequence of human pancreatic
                                                                                                                                                                                                                                                                                                                                1;
                                                                                                                                                                                                                                                                                                            DB 1; Length 263;
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A 7AAC699A0A64FBB CRC64;
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                                                                                                                                                CHYMOTRYPSIN A.
CHARGE RELAY SYSTEM (
CHARGE RELAY SYSTEM (
CHARGE RELAY SYSTEM (
                                                                                                                                                                                                                                                                                                                                57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     231
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                                                                                                                                                                                                                                                                                                          57.5%; Score 701.5; DB 1
58.6%; Pred. No. 1.3e-53;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
CTymotrypsinogen B precursor (EC 3.4.21.1).
CTRB1 OR CTRB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         263 AA
                                                                                                                                                                                                                                                                                                                               33; Mismatches
email to license@isb-sib.ch)
                                                                                                                                                                                      BY
BY
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BY
S
                                                                                                                                                                                                                                                                                         28294 MW:
                  EMBL; X78490; CAA55242.1; -. HSSP; P00766; 1CHG.
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                                                                                                                                                                                                                                                                                                                                129; Conservative
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                                                                                                                                                263
75
120
213
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263 AA;
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                                                                                                                                                                                                                                                                                                                      Similarity
                                      MEROPS; S01.152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTRB_HUMAN
P17538;
or send an
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ACT_SITE
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DISULFID
DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGSLISQSWVVTAAHCNVSPGRHFVVLGEYDRSSNAEPLQVLSVSRAITHPSWNSTTMNN 120
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                                                                              Strausberg R.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: Preferential cleavage: Tyr-|-Xaa, Trp-|-Xaa,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHYMOTRYPEIN B, A CHAIN.
CHYMOTRYPEIN B, B CHAIN.
CHYMOTRYPEIN B, C CHAIN.
CHAMGE RELAY SYSTEM (BY SIMILARITY).
CHAMGE RELAY SYSTEM (BY SIMILARITY).
CHAMGE RELAY SYSTEM (BY SIMILARITY).
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1 18
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les 67; Indels
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4C1C055A490B8701 CRC64;
Biochem. Biophys. Res. Commun. 158:569-575(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHYMOTRYPSINGEN B.
                                                                                                                                           Phe-|-Xaa, Leu-|-Xaa.
-!- SUBCELLULAR LOCATION: Extracellular.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 1.46
35; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56.5%; Score 689.5; 55.4%; Pred. No. 1.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Interpro; IPR001314; Chymotrypsin.
Interpro; IPR001254; Ser_protease_Try.
Pfam, PP00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SWART; SW00020; Tryp_SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_HIS; 1.
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27870 MW;
                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M24400; AAA52128.1; -.
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PIR; A31299; A31299.
HSSP; P00766; 1CHG.
MEROPS; S01.152;
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MIM; 118890; -.
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154
186
209
263 AA;
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Matches 128; Conserv
                                       SEQUENCE FROM N.A.
                                                             TISSUE-Pancreas;
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34
167
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Smillie L.B., Furka A., Nagabhushan N., Stevenson K.J., Parkes C.O.; "Structure of chymotrypsinogen B compared with chymotrypsinogen A and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        139 PVCLASSNEALTEGLTCVTTGWGRLSGVGNVTPAHLQQVALPLVTVNQCRQYWDSSITDS 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120 DITLLKLATPAQFSETVSAVCLPNVDDDFPPGTVCATTGWGKTKYNALKTPEKLQQAALP 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79 SPGRHFVVLGEYDRSSNAEPLQVLSVSRAITHPSWNSTTMNNDVTLLKLASPAQYTTRIS 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19 CGIPAIKPALSFSQRIVNGENAVLGSWPWQVSLQDSSGFHFCGGSLISQSWVVTAAHCNV 78
                                                                                                                                                                                                                                                                                                                                                                                 Value 218:343-346(1968).

-!- CATALYTIC ACTIVITY: Preferential cleavage: Tyr-|-Xaa, Trp-|-Xaa, Phe-|-Xaa, Leu-|-Xaa, Location: Extracellular.
-!- DATABASE: NAME=Worthington enzyme manual;
-!- MATABASE: NAME=Worthington-biochem.com/manual/C/CHY.html".
PIR; A00953; KYBOB.
                                                                                                                                                                                                                         Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 | CGVPAIQPVLSGLARIVNGEDAVPGSWPWQVSLQDSTGFHFCGGSLISEDWVVTAAHCGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 LVTVNQCRQYWDSSITDSMICAGGAGASSCQGDSGGPLVCQKGNTWVLIGI 231
                                             25755 MW; 678016446FF5FEB5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54.6%; Score 666.5; DB 1;
57.3%; Pred. No. 1.3e-50;
iive 28; Mismatches 62;
                                                                                                                                                                          21-JUL-1986 (Rel. 01, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Chymotrypsinogen B (EC 3.4.21.1).
                                                                                                                                    245 AA
                                                                                                                                                                                                                                                                                                               SEQUENCE, DISULFIDE BONDS, AND ACTIVE SITE.
                                                                                                                                                                                                                                                                                                                             MEDLINE-68238908; PubMed-5649671,
                                                                                                                                                                 21-JUL-1986 (Rel. 01, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                     Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP; P00766; 1ACB. MEROPS; S01.152; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             245 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                   NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                        trypsinogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122;
                                                                                                                                  CTRB_BOVIN
P00767;
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ACT_SITE
ACT_SITE
DISULFID
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DISULFID
DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 GGSLISQSWVVTAAHCNVSPGRHFVVLGEYDRSSNAEPLQVLSVSRAITHPSWNSTTMNN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 GGSLISEDWVVTAAHCGVKTS-DVVVAGEFDQGSDEENIQVLKIAQVFKNPKFNMFTVRN 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 DVTLLKLASPAQYTTRISPVCLASSNEALTEGLTCVTTGWGRLSGVGNVTPAHLQQVALP 180
                                                                                                                      Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MAFLWLVSCFALVGATFGCGVPTIQPVLTGLSRIVNGEDAIPGSWPWQVSLQDKTGFHFC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MILLSLTLSLVLLGSSWGCGIPAIKPALSFSQRIVNGENAVLGSWPWQVSLQDSSGFHFC 60
                                                                                                                                                                                                                                     "ISOLATION and sequence of a rat chymotrypsin B gene.";
J. Biol. Chem. 259:14265-14270(1984).
-!- CATALYTIC ACTIVITY: Preferential cleavage: Tyr-|-Xaa, Trp-|-Xaa,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHYMOTRYPSIN B, A CHAIN.
CHYMOTRYPSIN B, B CHAIN.
CHYMOTRYPSIN B, C CHAIN.
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEROPS, S01.152; ---
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001354; Ser_protease_Try.
InterPro; IPR001254; Ser_protease_Try.
PRIMTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPC; 1.
SMART; SM00020; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_DOM; 1.
PROSITE; PS00135; TRYPSIN_BS; 1.
Hydrolase; Serine protease; Digestion; Pancreas; Zymogen; Signal.
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                                                                                                                                                                 [1]
SEQUENCE FROM N.A.
MEDLINE-85054881; PubMed=6209274;
Bell G.I., Quinto C., Quiroga M., Valenzuela P., Craik C.:
Rutter W.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACAFDBACF8C4DA6D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHYMOTRYPSINGGEN B.
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                                          01-APR-1988 (Rel. 07, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Chymotrypsinogen B precursor (EC 3.4.21.1).
    263 AA
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    PRT;
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                                 (Rel. 07, Created)
(Rel. 07, Last seq
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   STANDARD;
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                                                                                                        Rattus norvegicus (Rat).
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HSSP; P00766; 1CHG.
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                                                                                                                                                NCBI_TaxID=10116;
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19
19
167
175
120
213
19
60
60
154
                               01-APR-1988
                                                                                                                                     Mammalia;
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ACT_SITE
ACT_SITE
ACT_SITE
DISULFID
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1;

Gaps

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Indels

Length 245;

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79 SPGRHFVVLGEYDRSSNAEPLQVLSVSRAITHPSWNSTTMNNDVTLLKLASPAQYTTRIS 138
                                                      PVCLASSNEALTEGLTCVTTGWG--RLSGVGNVTPAHLQQVALPLVTVNQCRQYW-DSSI 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF CHYWOTRYPSINOGEN.
MEDLINE-70177557; PubMed-5442169;
Freer S.T., Kraut J., Robertus J.D., Wright H.T., Xuong N.H.;
"Chymotrypsinogen: 2.5-A crystal structure, comparison with alpha-
chymotrypsin, and implications for zymogen activation.";
Biochemistry 9:1997-2009(1970).
                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                               electrophoresis.
A.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE, AND DISULFIDE BONDS.
MEDLINE-67183948; PubMed-5972866;
Meloun B., Kluh I., Kostka V., Moravek L., Prusik Z., Vanacek J.,
Keil B., Sorm F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alpha-chymotrypsin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-72035052; Pubmed-4399050; BirKroft J.J., Blow D.M., Henderson R., Steitz T.A.; Blow D.M., Henderson R., Steitz T.A.; Estine proteinases Structure of alpha-chymotrypsin. Philos. Trans. R. Soc. Lond., B. Biol. Sci. 257:67-76(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Smillie L.B., Hartley B.S.; "Histidine sequences in the active centres of some 'serine'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-69106266; Pubmed-5764436;
Blow D.M., Birktoft J.J., Hartley B.S.;
"Role of a buried acid group in the mechanism of action
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Amino-acid sequence of bovine chymotrypsinogen-A.";
Nature 201:1284-1287(1964).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Covalent structure of bovine chymotrypsinogen A.";
Biochim. Biophys. Acta 130:543-546(1966).
                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-67181721; PubMed-5971783; BEOWN J.R., Hartley B.S., Location of disulphide bridges by diagonal paper The disulphide bridges of bovine chymotrypsinogen
                                                                                                                                     212
                                                                                                                                                                                                                             21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                          196 TDSMICAGGAGASSCQGDSGGPLVCQKGNTWVLIGI 231
                                                                                                                                                                                                       245 AA
                                                                                                                       SDVMICAGAAGATSCMGDSGGPLVCQKDNVWTLVGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-67181723; PubMed-5971785;
                                                                                                                                                                                                                                                                        Chymotrypsinogen A (EC 3.4.21.1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biochem. J. 101:232-241(1966).
                                                                                                                                                                                                                                                                                                                                                                                                                                       Biochem. J. 101:214-228(1966).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 221:337-340(1969).
                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X-RAY CRYSTALLOGRAPHY.
                                                                                                                                                                                                                                                                                                                              Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY SEQUENCE.
                                                                                                                                                                                                                                                                                        Bos taurus (Bovine)
                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID-9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REVISION TO 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hartley B.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chymotrypsin.
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                                                                                                                                                                                                     CTRA_BOVIN
P00766;
                                                                                                                                                                                           CTRA_BOVIN
                                                      139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Chymntrypain B (EC 3.4.21.1)
Gadus morhua (Atlantic Cod).
Eukaryota; Metacaoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Gadus.
                                                                                                                                                                                                                                                                                                  Leth-Larsen R., Asgeirsson B., Thorolfsson M., Noerregaard-Madsen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hydrolase; Serine protease; Digestion; Pancreas; Zymogen.
CHAIN 16 245 CHYMOTRYPEIN B, A CHAIN.
CHAIN 16 245 CHYMOTRYPEIN B, B CHAIN.
ACT_SITE 57 57 CHARGE RELAY SYSTEM (BY SIMILARITY).
ACT_SITE 101 101 CHARGE RELAY SYSTEM (BY SIMILARITY).
ACT_SITE 195 195 CHARGE RELAY SYSTEM (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7;
                                                                                                                                                                                                                                                                                                                           Structure of chymotrypsin variant B from Atlantic cod, Gadus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              245;
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S -> T (IN REF. 2).
PW -> Y (IN REF. 2).
74FE0D425517AB02 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54.4%; Score 664.5; DB 1
58.3%; Pred. No. 1.9e-50;
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BY SIMILARITY.

BY SIMILARITY.

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BY SIMILARITY.
                                                                                            245 AA
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199 MICAGGAGASSCQGDSGGPLVCQKGNTWVLIGI 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00089; trypain; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM0020; Tryp_SPc; 1.
PROSITE; PS00144; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
                                                                                                                                                                                                                                                                                                                                                      Biochim. Biophys. Acta 1297:49-56(1996)
               180 MICAGASGVSSCMGDSGGPLVCQKNGAWTLAGI
                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-92111252; PubMed-1764912;
                                                                                                                                                                                                                                                                                   MEDLINE-96439045; PubMed-8841380;
                                                                                                                    01-OCT-1996 (Rel. 34, Created)
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                                                                                            STANDARD;
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101
195
195
121
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201
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220
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245 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEROPS; S01.152;
                                                                                                                                                                                                                               NCBI_TaxID-8049;
                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Pyloric
                                                                                                                                                                                                                                                                                                                Hoejrup P.;
                                                                                           CTRB_GADMO
P80646;
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ACT_SITE
ACT_SITE
DISULFID
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SEQUENCE
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                                                                                                                                                                                                                                                        SEQUENCE
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                                                                              GADMO
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79 SPGRHFVVLGEYDRSSNAEPLQVLSVSRAITHPSWNSTIMNNDVTLLKLASPAQYTTRIS 138
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                                                                                                                                                                                                                                                                                                                                                                                                                         53.8%; Score 657.5; DB 1; ilarity 54.9%; Pred. No. 7.5e-50; Conservative 37; Mismatches 58;
 CHARGE RELAY SYSTEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MICAGGAGASSCQGDSGGPLVCQKGNTWVLIGI 231
245 AA;
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                                   resolution.
                                                                  X-RAY CRYSTALLOGRAPHY (1.68 ANGSTROMS) OF ALPHA-CHYMOTRYPSIN. MEDLINE=86011575; PubMed=4046030; Tsukada H., Blow D.M.; "Structure of alpha-chymotrypsin refined at 1.68-A resolution."; J. Mol. Biol. 184:703-711(1985).
                                                                                                                   Phe-!-Xaa, Leu-!-Xaa.
-:- SUBCELLOUAR LOCATION: Extracellular.
-!- SUMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
-!- DATABASE: NAME-Worthington enzyme manual;
WWW-"http://www.worthington-biochem.com/manual/C/CHY.html".
       X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF GAMMA-CHYMOTRYPSIN MEDLINE-82078042; PubMed-6914398; Cohen G.H., Silverton E.W., Davies D.R.; Refined crystal structure of gamma-chymotrypsin at 1.9-A reComparison with other pancreatic serine proteases."; J. Mol. Biol. 148:449-479(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lydrolase; Serine protease; Digestion; Pancreas; Zymogen;
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CHYMOTRYPSIN A, B CHAIN.
CHYMOTRYPSIN A, C CHAIN.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
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SMOSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_ESER; 1.
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PRINTS; PR00722; CHYMOTRYPSIN.
                                                                                                                                                                    2CGA; 15-APR-90.

2CHA; 31-MAY-84.

5CHA; 16-OCT-87.

6CHA; 16-OCT-87.

1CHG; 27-JAN-84.

1CHG; 27-JAN-84.

1CHG; 27-JAN-84.

1CHG; 15-OCT-90.

5GCH; 15-OCT-90.

6GCH; 15-OCT-90.

6GCH; 15-OCT-90.

6GCH; 15-OCT-90.

6GCH; 15-OCT-91.

2GCT; 15-OCT-91.

3GCT; 15-OCT-91.

3GCT; 15-OCT-91.

3GCT; 15-OCT-91.
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146
245
57
102
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PDB, 4CHA, 29-0CT-85
PDB, 5CHA, 16-0CT-87
PDB, 5CHA, 16-0CT-87
PDB, 1CHO, 16-0LL-88
PDB, 1CHO, 16-0LL-88
PDB, 3CCH, 15-0CT-92
PDB, 4CCH, 15-0CT-92
PDB, 5CCH, 15-0CT-90
PDB, 5CCH, 15-0CT-90
PDB, 5CCH, 15-0CT-91
PDB, 1CCH, 13-0CT-91
PDB, 1CCH, 13-0CH-97
PDB, 1CCH, 23-0LL-97
PDB, 1CCH, 23-0LL-97
PDB, 1CCH, 23-0LL-97
PDB, 1CCH, 23-0CH-97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i- FUNCTION: ACTS UPON ELASTIN.
-i- CATALYTIC ACTIVITY: Preferential cleavage: Leu-|-Xaa, Met-|-Xaa and Phe-|-Xaa. Hydrolyzes elastin.
-i- SUBCELLULAR LOCATION: Secreted.
-i- TISSUE SPECIFICITY: PANOREAS.
-i- TISSUE SPECIFICITY: PANOREAS.
                                                                                                                                                                                                                                                                                                                                              Kawashima I., Tani T., Shimoda K., Takiguchi Y.; "Characterization of pancreatic elastase II cDNAs: two elastase II mRNAs are expressed in human pancreas.";
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Sus.
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Shirasu Y., Yoshida H., Matsuki S., Takemura K., Ikeda N.,
Shimada Y., Ozawa T., Mikayama T., Iijima H., Ishida A., Sato Y.,
Tamai Y., Tanaka J., Ikenaga H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Molecular cloning and expression in Escherichia coli of a cDNA
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                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
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L -> S (IN REF. 2).
N -> K (IN REF. 2).
S -> Y (IN REF. 2).
C -> V (IN REF. 2).
C -> V (IN REF. 2).
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                                                                   01-AUG-1988 (Rel. 08, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Elastase 2 precursor (EC 3.4.21.71).
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SMART; SM00020; TRYP_SPC; 1.
PROSITE; PSS0140; TRYPSIN_DOM; 1.
PROSITE; PS00144; TRYPSIN_LOM; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
Hydrolase; Serine protease; Zymogen; Signal.
  269 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          encoding human pancreatic elastase 2.";
J. Biochem. 102:1555-1563(1987).
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InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00089; trypsin; 1.
                                                                                                                                                                                                                                                                                                                           MEDLINE-87217962; PubMed-3646943;
                                                 (Rel. 08, Created)
(Rel. 08, Last seq
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EMBL; D00237; BAA00166.1; -.
PIR; A26823; A26823.
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  STANDARD;
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269 AA;
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MEROPS; S01.155; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                         Sus scrofa (Pig)
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                                              01-AUG-1988
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MEDLINE-8998996; PubMed-2737288;
Wendorf P., Geyer R., Sziegoleit A., Linder D.;
"Localization and characterization of the glycosylation site of human pancreatic elastase 1.";
Pancreatic elastase 1.";
FEBS Lett. 249:275-278(1989).
-i- FUNCTION: EFFICIENT PROTEASE WITH ALANINE SPECIFICITY BUT ONLY LITTLE ELASTOLYTIC ACTIVITY.
                                                                                                                                  59 FCGGSLISQSWVVTAAHCNVSPGRHFVVLGEYDRSSNAEPLQVLSVSRAITHPSWNSTTM 118
                                                                                                                                                   N - - NDVTLLKLASPAQYTTRISPVCLASSNEALTEGLTCVTTGWGRLSGVGNVTPAHLQQ 176
                                                                                                                                                                                                                      Gaps
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MEDLINE-88087253; PubMed=2826474;
Tani T., Obsumi J., Mita K., Takiquchi Y.;
Identification of a novel class of elastase isozyme, human panorreatic elastses III, by CDNA and genomic gene cloning.";
J. Biol. Chem. 263:1231-1239(1988).
 Length 269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                    84; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                 16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Elastase IIIB precursor (EC 3.4.21.70) (Protease
 Score 472; DB 1;
Pred. No. 8.9e-34;
2; Mismatches 84.
                                                                                                                                                                                                                                                                                                                                                                                  270 AA
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Shen W., Fletcher T.S., Largman C.;
"Primary structure of human pancreatic psequence analysis of the cloned mRNA.";
Biochemistry 26:3447-3452(1987).
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MEDLINE-89325560; PubMed-2753124;
                                32;
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38.7%;
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                                Matches 109; Conservative
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MEROPS; S01.155;
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01-NOV-1997
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                                                                       EL2_BOVIN
Q29461;
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                                                                                           SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                       between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. ELASTASE SUBFAMILY. CAUTION: Was originally (Ref.5) thought to be elastase 1.
-!- CATALYTIC ACTIVITY: Preferential cleavage: Ala-|-Xaa. Does not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hydrolase; Serine protease; Zymogen; Signal; Glycoprotein.
SIGNAL 1 15 OR 16 (POTENTIAL).
PROPEP 16 28 ACTIVATION PEPTIDE (POTENTIAL).
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R -> P (IN REF. 3).
B14BE0AAD3695AFE CRC64;
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A -> G (IN REF. 3).
W -> R (IN REF. 1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro: IPR001314; Chymotrypsin.
InterPro: IPR001254; Ser_protease_Try.
Pfam; PP00089; trypsin.
SMART; SM00020; Trypsin.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS50240; TRYPSIN_LOM; 1.
PROSITE; PS00134; TRYPSIN_LOM; 1.
PROSITE; PS00134; TRYPSIN_LSER; 1.
                                                                                                                                                                                                                                            EMBL; M16630; AAA36482.1; -.
EMBL; BC005216; AAH05216.1; -.
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                                                                                                                                                                                                                                                                                  EMBL; M18692; AAA58454.1; -...
PIR, B29934, B29934.
PIR, S047206; A77206.
PIR, S04999; S04999.
PIR, S04490. S04490.
HSSP; P05805; IFON.
MEROPS; S01.205; -...
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nes 102; Conservative
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                 hydrolyse elastin.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-98079203; PubMed=9418008; Gestin M., le Huerou-Luron I., Wicker-Planquart C., le Drean G., Chaix J.C., Puigserver A., Guilloteau P.; "Bovine pancreatic preproelastases I and II: comparison of nucleotide and amino acid sequences and tissue specific expression."; comp. Biochem. Physiol. 1188:181-187(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --- CATALYTIC ACTIVITY: Preferential cleavage: Leu-|-Xaa, Met-|-Xaa and Phe-|-Xaa. Hydrolyzes elastin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -1- TISSUE SPECIFICITY: PANCREAS.
-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. ELASTASE SUBFAMILY.
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                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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ACTIVATION PEPTIDE (BY SIMILARITY).
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InterPro; IPR001254; Ser_protease_Try.
Pfam; PP00089; Trypsin; 1.
PRNTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS5040; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_LHS; 1.
PROSITE; PS00135; TRYPSIN_LHS; 1.
PROSITE; PS00135; TRYPSIN_ERR; 1.
Hydrolase; Serine protease; Zymogen; Signal.
                                                   1-NOV-1997 (Rel. 35, Created)
1-NOV-1997 (Rel. 35, Last sequence update)
5-JUN-2002 (Rel. 41, Last annotation update)
1astase 2 precursor (RC 3.4.21.71).
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STANDARD;
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269 AA;
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117 AQGNDIALLKLASSVPLTDKIQLGCLPAAGTILPNNYVCXVTGWGRLQSNG-ALPDILGO 175
                                                                   -- NNDVTLLKLASPAQYTTRISPVCLASSNEALTEGLTCVTTGWGRLSGVGNVTPAHLQO 176
                                                                                                                                                            177 VALPLVTVNQCR--QYWDSSITDSMICAGGAG-ASSCQGDSGGPLVCQKGN-TWVLIGI 231
                                                                                                                                                                                       | :| | :| | : | | : | | 134 | 135 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 134 | 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg R.;
Submitted (ApR-2001) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: ACTS UPON ELASTIN.
-I- CATALYTIC ACTIVITY: Preferential cleavage: Leu-|-Xaa, Met-|-Xaa
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-- SUBCELULAR LOCATION: Secreted.
--- TISSUE SPECIFUCIT: PANCHEAS.
--- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. ELASTASE SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kawashima I., Tani T., Shimoda K., Takiguchi Y.;
"Characterization of pancreatic elastase II cDNAs: two elastase II
mRNAs are expressed in human pancreas.";
DNA 6:163-172(1987).
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Catarrhini; Hominidae; Homo.
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Shirasu Y., Yoshida H., Matsuki S., Takemura K., Ikeda N., Shim
Ozawa T., Mikayama T., Iijima H., Ishida A., Sato Y., Tamai Y.,
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Fletcher T.S., Shen W.F., Largman C.;
"Primary structure of human parnreatic elastase 2 determined lasquence analysis of the cloned mRNA.";
Biochemistry 26:7256-7261(1987).
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Last annotation update)
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01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
Elastase 2A precursor (EC 3.4.21.71).
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Mammalla; Eutheria; Primates;
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N--NDVTLLKLASPAQYTTRISPVCLASSNEALTEGLTCVTTGWGRLSGVGNVTPAHLQQ 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Muriņae; Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                   ACTIVATION PEPTIDE.
ELASTASE 2A.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
CHARGE RELAY SYSTEM (BY SIMILARITY).
C -> V (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [1] SEQUENCE FROM N.A. MEDLINE-8218221; McDonald R.J., Swift G.H., Quinto C., Swain W., Pictet R.L., McDonald R.J., Swift G.H., Quinto C., Swain W., Pictet R.L., Nikovits W., Rutter W.J.; in the conformal structure of two distinct rat pancreatic preproclastases determined by sequence analysis of the complete cloned messenger ribonucleic acid sequences."; Biochemistry 21:1453-1463(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 LLLSLTLSLVLLGSSWGCGIPAIKPALSFSQRIVNGENAVLGSWPWQVSLQDSSG---FH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36.4%; Score 445; DB 1; Length 269; 43.9%; Pred. No. 1.9e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A2E05143EFF4987C CRC64;
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15-JUN-2002 (Rel. 41, Last annotation update)
Elastase 2 precursor (EC 3.4.21.71).
                                                                                                                                                                                                                                                                                     PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE: PS00135; TRYPSIN_SER; 1.
Hydrolase; Serine protease; Zymogen; Signal.
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                                                                                                                                                                          InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28;
                                                                                                                                                                                                                      Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Rel. 01, Created)
(Rel. 01, Last sequ
(Rel. 41, Last anno
                                  EMBL; AL512883; CAC42421.1; -. EMBL; BC007031; AAH07031.1; -. PIR; A27432; A27432.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28888 MW;
  AAA52380.1; -.
BAA00165.1; -.
M16652; AAA52380.1;
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                                                                                                                                HSSP; P00772; 1ELG. MEROPS; S01.155; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   269 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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21-JUL-1986 (
15-JUN-2002 (
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DISULFID
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178 GRLLVVDYATCSSASWWGSSVKTNMVCAGGDGVTSSCNGDSGGPLNCQASNGQWQVHGI 236

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RESULT 14
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                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                           modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59 TCGGSLVANNWVLTAAHCISNSRTYRVLLGRHSLSTSESGSLAVQVSKLVVHEKWNAQKL 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59 FCGGSLISQSWVVTAAHCNVSPGRHFVVLGEYDRSSNAEPLQVLSVSRAITHPSWNSTTM 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119 N--NDVILLKLASPAQYTTRISPVCLASSNEALTEGLTCVTTGWGRLSGVGNVTPAHLQQ 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   177 VALPLVTVNQC - - RQYWDSSITDSMICAGGAG - ASSCQGDSGGPLVCQKGN - TWVLIGI 231
                                                                        BIOL. Chem. 259:14271-14278(1984).
FUNCTION: ACTS UPON ELASTIN.
- CATALITIC ACTIVITY: Preferential cleavage: Leu-|-xaa, Met-|-xaa and Phe-:-xaa. Hydrolyzes elastin.
- SUBCELLULAR LOCATION: Secreted.
                                                                                                                                 TISSUE SPECIFICITY: PANCREAS.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. ELASTASE SUBFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 LLLSLTLSLVLLGSSWGCGIPAIKPALSFSQRIVNGENAVLGSWPWQVSLQD-SSG--FH
                                 Swift G.H., Craik C.S., Stary S.J., Quinto C., Lahaie R.G.,
Rutter W.J., Macdonald R.J.;
"Structure of the two related elastase genes expressed in the rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY).
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SIMILARITY)
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                               Stary S.J., Quinto C., Lahaie R.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               125C783B857B71E3 CRC64;
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CHARGE RELAY SYSTEM
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Pred. No. 7.8e-31;
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SIMILARITY.
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InterPro; IPR001254; Ser_protesse_Try.
Pram; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM0020; Tryp_SPC; 1.
PROSITE; PS00404; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_ESR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35.9%; Score 438;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ELASTASE
                     MEDLINE-85054882; PubMed-6094548;
Swift G.H., Craik C.S., Stary S.J
                                                                                                                                                                                                                                                                                         AAA98780.1; JOINED. AAA98780.1; JOINED.
                                                                                                                                                                                                                                                                              AAA98780.1; JOINED.
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AAA98780.1;
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Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                            1ELG.
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HSSP; P00772; 1ELG
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218
60
157
1188
214
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                                                                 pancreas."
J. Biol. C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                    -1- TISSUE SPECIFICITY: PANCREAS.
-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. ELASTASE SUBFAMILY
                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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CHARGE RELAY SYSTEM
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; Pred. No. 6.9e-30;
36; Mismatches 91
                                                                       01-AUG-1988 (Rel. 08, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Elastase 2B precursor (EC 3.4.21.71).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PRO0722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
HYDROSTE; PS00135; TRYPSIN_SER; 1.
Hydrolase; Serine protease; Zymogen; Signal.
                   269 AA
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InterPro; IPR001254; Ser_protease_Try.
                   PRT;
                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE-87217962; PubMed-3646943;
                                                       08, Created)
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41.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 41.0%
                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00089; trypsin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121
                                                                                                                                  (Human)
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; P05805; 1FON.
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212
269 AA;
                                                     01-AUG-1988 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; P05805; 1FC
MEROPS; S01.206;
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216
58
155
                                                                                                                               Homo sapiens
                   EL2B_HUMAN
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ACT_SITE
DISULFID
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CHAIN
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EL2B_HUMAN
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               119 N--NDVTLLKLASPAQYTTRISPVCLASSNEALTEGLTCVTTGWGRLSGVGNVTPAHLQQ 176
                                                                            LITTLE ELASTOLYTIC ACTIVITY.
-!- CATALYTIC ACTIVITY: Preferential cleavage: Ala-|-Xaa. Does not hydrolyse elastin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. ELASTASE SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (APR-2001) to the EMBL/Genbank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-89034017; pubMed-2460440;
Shirasu Y. Takemura K., Yoshida H., Sato Y., Iijima H.,
Shinada Y., Mikayama T., Ozawa T., Ikeda N., Ishida A., Tamai Y.,
Matsuki S., Tanaka J., Ikenaga H., Ogawa M.;
Molecular cloning of complementary DNA encoding one of the human
pancreatic protease E isozymes.";
Blochem. 104:259-264(1988).
                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                           177 VALPLVTVNQCRQ--YWDSSITDSMICAGGAGA-SSCQGDSGGPLVCQKGN-TWVLIGI
                                                                                                                                                                                                                                                                                                                                                                                                Tani T., Ohsumi J., Mita K., Takiguchi Y.;
"Identification of a novel class of elastase isozyme, human
pancreatic elastase III, by CDNA and genomic gene cloning.";
J. Biol. Chem. 263:1231-1239(1988).
                                                                                                                                                                 EL3A_HUMAN STANDARD; PRT; 270 AA. P09093; Q9BRW4; P00093; Q9BRW4; Q01-MAR-1999 (Rel. 10, Created) Q1-FEB-1996 (Rel. 33, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Elastase IIIA precursor (EC 3.4.21.70) (Protease E).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-88087253; PubMed-2826474;
                                                                                                                                                                                                                                                                          Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Pancreas;
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58 HFCGGSLISQSWVVTAAHCNVSPGRHFVVLGEYDRSSNAEPLQVLSVS--RAITHPSWNS 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 174 LQQVALPLVTVNQCRQ--YWDSSITDSMICAGGAGASSCQGDSGGPLVC-QKGNTWVLIG 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       116 SCVACGNDIALIKLSRSAQLGDAVQLASLPPAGDILPNKTPCYITGWGRLYTNGPL-PDK 174
                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                              2 MLRLLSSLLLVAVASGYG-----PPSSHSSRVVHGEDAVPYSWPWQVSLQYEKSGSFY 55
                                                                                                                                                                       CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
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PROBABLE.
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                                                                                                                                      OR 16 (POTENTIAL).
ACTIVATION PEPTIDE (POTENTIAL).
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001314; Ser_protease_Try.
Pfam: PF00089; trypsin; 1.
PR1NTS; PR00722; CHYMOTRYPSIN.
SMRT; SM00200; Tryp_SPro; 1.
PROSITE; PS00134; TRYPSIN_EN; 1.
PROSITE; PS00134; TRYPSIN_EN; 1.
PROSITE; PS00135; TRYPSIN_EN; 1.
Hydrolase; Serine protease; Symogen; Signal; Glycoprotein.
SIGNAL
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I -> T (IN REF. 3).
MISSING (IN REF. 1).
K -> E (IN REF. 3).
                                                                                                                                                               ELASTASE IIIA.
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Job time : 8.91304 secs
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Watches 98; Conserv
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ACT_SITE
DISULFID
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Sequence 363, App Sequence 363, App Sequence 363, App Sequence 363, App Sequence 363, App Sequence 363, App Sequence 363, App Sequence 363, App Sequence 363, App Sequence 242, App Sequence 2, App11 Sequence 2, App11 Sequence 1, App1 Sequence 1, App11 equence 32, A
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APPLICANT: Rosen et al.
TITLE OF INVENTION:
FILE REFERENCE: PAIGO 5001-08-10
CURRENT APPLICATION NUMBER: US/09/925,297
CURRENT APPLICATION NUMBER: US/09/925,297
CURRENT APPLICATION NUMBER: PCT/US00/05989
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR SED ID 805: 928
NUMBER OF SEQ ID NOS: 928
SOFFWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                               US-10-010-928-2

US-09-802-124-2

US-09-73-605-2

US-09-746-284-1

US-09-746-284-1
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86.2%; Pred. No. 2e-10;
tive 3; Mismatches 1;
            US-10-063-547-66
US-99-092-296-15
US-09-989-722-363
US-09-989-727-363
US-09-989-727-363
US-09-989-727-363
US-09-989-727-363
US-09-991-073-363
US-09-991-073-363
US-09-991-053-363
US-09-991-163-363
US-09-989-721-363
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US-10-063-547-32
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Patent No. US20020081659A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 96, Application US/09888615; Patent No. US20020064856A1
GENERAL INFORMATION: APPLICANT: PLOWMAN, GREGORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WHYTE, DAVID
CAENEPEEL, SEAN
CHARYDCZAK, GLEN
MANNING, GERARD
SUDARSANAM, SUCHA
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Best Local Similarity
US-09-925-297-529
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LENGTH: 192
TYPE: PRT
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US-09-888-615-96
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APPLICANT:
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Sequence 643, Appl
Sequence 2, Appl1
Sequence 2, Appl1
Sequence 1, Appl1
Sequence 12, Appl1
Sequence 12, Appl1
Sequence 11, Appl
Sequence 671, Appl
Sequence 671, Appl
Sequence 679, Appl
Sequence 224, Appl1
Sequence 7, Appl1
                                                                                                                                                            (without alignments)
530.147 Million cell updates/sec
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                                                                                                                                       December 20, 2002, 15:16:49; Search time 1.04348 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cgn2_6/ptodata/1/pubpaa/USOB_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/USOG_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/USOG_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/USOG_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/USOT_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/USOZ_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/USOB_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/USOB_PUBCOMB.pep:*
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/cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*
                 GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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0 US-09-92-647-12

0 US-09-860-677-118

0 US-09-764-883-671

0 US-09-764-883-679

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                                                                                                                                                                                                                                                                                                                                                                      106657 seqs, 16763532 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Published_Applications_AA:*
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Maximum Match 100%
Listing first 45 summaries
                                                                                                - protein search, using sw model
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166
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match Length
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47.5
47.5
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No.
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16 LVGAAFGCGVPAIHPVLS 33
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US-09-448-378-2
                                                                                           US-10-095-449-2
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                                                                   RESULT 4
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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Fatent No. US20020081659A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION:
FILE REFERENCE: PA105
CURRENT APPLICATION NUMBER: US/09/925, 297
CURRENT APPLICATION NUMBER: D01-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05989
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 928
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 643
LENGTH: 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 67; DB 10; Length 146; Pred. No. 0.053; 4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                            DB 10; Length 263;
                                                                                                                                                                                                                                                                                                                        41.0%; Score 68; DB 10; Length 26 nilarity 51.7%; Pred. No. 0.073; Conservative 4; Mismatches 10; Indels
            FILE REFERENCE: 038602/1214
CURRENT APPLICATION NUMBER: US/09/888,615
CURRENT FILING DATE: 2001-06-26
PRIOR APPLICATION NUMBER: 60/214,047
NUMBER OF SEQ ID NOS: 150
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                      1 MLLLSLTLSLVLLGSSWGCGVPAITPALS 29
                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: NOVEL PROTEASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 40.4%;
Best Local Similarity 66.7%;
Matches 12; Conservative
                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-888-615-96
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ORGANISM: Homo sapiens
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Matches 15; Conserv
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LOCATION: (2)
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12 LLGSSWGCGVPAITPALS 29 

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                                                                                                                                                                                       ADDRESSEE: Stephen L. Malaska, Immunex Corporation
STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 231;
                                                                                      Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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2836-D
                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Microsoft Word, Version #5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/095,449
FILING DATE: 13 Mar-2002
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33.1%; Score 55; DB 9;
61.1%; Pred. No. 3.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 08/669,692
FILING DATE: 24-7UN-1996
FILING DATE: December 3, 1993
APPLICATION NUMBER: 08/11/758
FILING DATE: August 25, 1993
APPLICATION NUMBER: 08/106,463
FILING DATE: August 25, 1993
APPLICATION NUMBER: 08/106,463
FILING DATE: August 12, 1993
FILING DATE: August 12, 1993
FILING DATE: MAY 24, 1993
                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Mismatches
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REFERENCE/DOCKET NUMBER: 2813-C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/09448378
Patent No. US20020034517A1
GENERAL INFORMATION:
APPLICANT: Brasel, Kenneth
TITLE OF INVENTION: Dendritic Cel
Sequence 2, Application US/10095449 Patent No. US20020160004A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 231 amino acids TYPE: amino acid
                                                                          APPLICANT: Lyman, Stewart D.
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192 LLLLLPLTLVLLAAAWG 209
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                                                                                                                                                                                                                                                                  STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MLLLSLTLSLVLLGSSWG 18
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Best Local Similarity 61.1'
Matches 11; Conservative
                                                                                                                                                                                                                                              CITY: Seattle
                                                                                                                                                                                                                                                                                        COUNTRY: US
                                                                                                                                                                                                                                                                                                                 ZIP: 98101
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APPLICANT: Xu, Hong
APPLICANT: Cohan, Victoria L.
APPLICANT: Cohan, Victoria L.
APPLICANT: Stuart, Suan G.
TITLE OF INVENTION: HUMAN EMRI-LIKE G PROTEIN-COUPLED RECEPTOR
FILE REFERENCE: PC-0052 CIP
CURRENT APPLICATION NUMBER: US/09/992,647
CURRENT FILING DATE: 2002-11-13
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PERL PROGRAM
SEQ ID NO 12
LENGTH: 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 55; DB 10; Length 242;
Pred. No. 3.3;
3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION UNMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR PRILING DATE: 2000-11-27
PRIOR PRILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-21-22
PRIOR FILING DATE: 2001-02-16
                                 Indels
            Pred. No. 3.1;
1; Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13730
LENGTH: 242
                                                                                                                                                                                                                                           Sequence 13730, Application US/09815242 Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 12, Application US/09992647
Patent No. US20020146767A1
GENERAL INFORMATION:
            Best Local Similarity 61.1%; Promatches 11; Conservative 4;
                                                                                                                                                                                                                                                                                                                                  APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
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58.8%;
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192 LLLLLPLTLVLLAAAWG 209
                                                                             1 MLLLSLTLSLVLLGSSWG 18
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APPLICANT: Haselbeck, Robert
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US-09-815-242-13730
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Best Local Similarity 58.8
Matches 10; Conservative
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STREET: 51 University Street
CITY: Seattle
COUNTY: Mashington
                                                                                                                                                                                                                                        Length 231;
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Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
CORRESPONDENCE: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                         3; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
OPERATING SYSTEM: Macintosh 7.0.1
SOFTWARE: Microsoft Word, Version #5.1
CURRENT APPLICATION NUMBER: US/09/983,806
FILING DATE: 25-Oct-2001
CLASSIFICATION: 530
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APPLICATION NUMBER: US/08/444,626
FILING DATE: 19-MAY-1995
APPLICATION NUMBER: US 08/162,407
FILING DATE: 03-DEC-1993
APPLICATION NUMBER: 08/111,758
FILING DATE: August 25, 1993
APPLICATION NUMBER: 08/106,463
FILING DATE: August 12, 1993
APPLICATION NUMBER: 08/068,394
                                                                                                                                                                                                                                                                                         Mismatches
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CURRENT APPLICATION NUMBER: US/09/448,378
CURRENT FILING DATE: 1999-11-23
'NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin version 3.0
SEQ ID NO 2
LENGTH: 231
                                                                                                                                                                                                                                           Score 55;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/09983806
Patent No. US20020107365A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 231 amino acids
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SEQUENCE CHARACTERISTICS:
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61.1%;
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Best Local Similarity 61.1
Matches 11; Conservative
                                                                                                                                            TYPE: PRT ORGANISM: Mus sp. US-09-448-378-2
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SOFTWARE: PERL Program
SEQ ID NO 1
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                                                             US-09-764-853-671
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APPLICANT: BJARNARGON, JON B.

TITLE OF INVENTION: FISH SERINE PROTEINASES AND THEIR PHARMACEUTICAL AND TITLE OF INVENTION: COSMETIC USE
FILE REPERENCE: 81691/284960
CURRENT APPLICATION NUMBER: US/10/036,371
PRIOR APPLICATION NUMBER: 09/411,688
PRIOR FILING DATE: 1999-10-12
PRIOR FILING DATE: 1999-10-12
PRIOR FILING DATE: 1999-10-12
PRIOR FILING DATE: 1999-10-12
PRIOR FILING DATE: 1999-10-12
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                         ; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Genbank ID No. US20020146767A1 92935597
US-09-992-647-12
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US-09-860-670-118
Sequence 118, Application US/09860670
Factor No. US20020165137A1
GENERAL INFORMATION:
TILLE OF INVENTION: NUCLEIC ACIDS, Proteins, and Antibodies
FILE REFERENCE: PA127P1
CURRENT APPLICATION NUMBER: US/09/860,670
CURRENT APPLICATION NUMBER: US/09/860,670
FILE REFERENCE: PA12 P1
FILE OF APPLICATION OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN 
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Pred. No. 37;
4; Mismatches 13; Indels
                                                                                                                                                   DB 10; Length 344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 48; DB 12; Length 13;
Pred. No. 1.2;
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                                                                                                                                                                                                                                          13; Indels
                                                                                                                                                                                                                                          4; Mismatches
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                                                                                                                                                              Score 50;
Pred. No.
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                                                                                                                                                                                                                                                                                                          1 MLLLSLTLSLVLLGSSWGCGVPAITPA 27
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Sequence 5, Application US/10036371
Patent No. US20020141987A1
GENERAL INFORMATION:
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37.0%;
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37.0%;
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81.8%;
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Best Local Similarity 37.0%
Matches 10; Conservative
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Best Local Similarity 81.8
Matches 9; Conservative
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sapiens
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Best Local Similarity
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US-10-036-371-5
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LENGTH: 13
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NUMBER OF SEQ ID NOS: 12
                                                                                                                          CURRENT APPLICATION NUMBER: US/09/764,853
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 939
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 611
LENGTH: 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/764,898
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 311
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Sequence 671, Application US/09764853
Patent No. US20020090672A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: P1206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 219, Application US/09764898
Patent No. US20020090673A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PJZ01
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37;
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Pred. No. 37;
4; Mismatches 13;
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ilarity 37.0%;
Conservative
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SEQ ID NO 219
LENGTH: 331
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                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Homo sapiens
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Best Local Similarity
Matches 10; Conserv
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Search completed: December 20, 2002, 15:21:07 Job time: 1.04348 secs

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Fatent No. US20020090672A1
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
CURRENT FILING DATE:
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 939
SEQ ID NO 679
LENGTH: 661
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Fatent No. US2002009067341
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE REFERENCE: PJZ01
CURRENT APPLICATION NUMBER: US/09/764,898
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper; NOWBER OF SEQ ID NOS: 311
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 224
LENGTH: 661
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                                                                                                                                                    Length 652;
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Best Local Similarity 37.0%; Pred. No. 76;
Matches .10; Conservative 4; Mismatches 13; Indels
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                                                                        ; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020146767A1 429905
US-09-992-647-1
                                                                                                                                                  Query Match
28.9%; Score 48; DB 10;
Best Local Similarity 37.0%; Pred. No. 75;
Matches 10; Conservative 4; Mismatches 13;
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LENGTH: 652
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
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CORGANISM: Homo sapiens
US-09-764-853-679
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US-09-764-853-679
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Sequence:

Title:

Searched:

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Sequence 14, Application US/09052778A

Patent No. 6060590

GENERAL INFORMATION:
APPLICANT: Bryant, Peter J.
APPLICANT: Bryant, Razuo
TITLE OF INVENTION: CHITINASE RELATED PROTEINS AND METHODS
TITLE OF INVENTION: OF USE
FILE REFERENCE: 07306/015001
CURRENT APPLICATION NUMBER: US/09/052,778A

CURRENT FILING DATE: 1998-03-31
NUMBER OF SEQ ID NOS: 16

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO. 14
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STATE: New York
COUNTRY: United States of America
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 3;
US-08-943-087-2
US-08-943-087-16
US-08-943-087-16
US-08-943-087-20
US-08-943-087-20
US-08-943-087-22
US-08-943-087-22
US-08-943-087-26
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US-08-943-087-40
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Patent No. 5525708
GENERAL INFORMATION:
APPLICANT: No. 5525708ka, Karl
APPLICANT: LObell, Robert B
TITLE OF INVENTION: STABILIZED DIMER OF KIT
COMBER OF SEQUENCES:
COMBERSEE: Fish & Neave
STREET: 1251 Avenue of the Americas
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Pred. No. 8.3;
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; ORGANISM: Drosophila melanogaster
US-09-052-778-14
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48.3%;
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 Best Local Similarity
Matches 14; Conserv
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519.349 Million cell updates/sec
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/cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
/cgn2_6/ptodata/1/1aa/fB_COMB.pep:*
/cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*
                 GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd
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US-08-160-841-2
US-09-160-841-2
US-09-160-841-2
US-08-24-05365-2
PCT-US94-05365-2
US-08-765-192-2
US-09-193-793-2
US-09-386-642-53
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US-09-386-642-53
US-09-110-116-4
US-09-116-116-1
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US-08-956-384-27
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US-09-10-116-1
US-09-10-10-089-2
US-09-670-827-2
US-09-670-827-2
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US-09-134-001C-3180
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Maximum Match 100%
Listing first 45 summaries
                                                                                         protein search, using sw model
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46.5
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Score 55; DB 1; Length 231;
Pred. No. 4.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Lyman, Stewart D.
APPLICANT: Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephen L. Malaska, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: Apple Macintosh
COMPUTER: Apple Macintosh
SOFTWARE: Microsoft Word, Version #5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/993,962
FILING DATE: December 18, 1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/162,407
FILING DATE: December 3, 1993
APPLICATION NUMBER: US/08/11,758
FILING DATE: AUGUST 25, 1993
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Mismatches
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/068,394
FILING DATE: MAY 24, 1993
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MAJASKA, Stephen L.
REFERENCE/DOCKET NUMBER: 2813-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEPHONE: (206) 233-0644
TELEPHONE: 756822
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 231 amino acids
TYPE: maino acids
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APPLICATION NUMBER: 08/106,463
FILING DATE: AUGUST 12, 1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION WIMBER: 08/068,394
FILING DATE: May 24, 1993
CLASSIFICATION: 424
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Patent No. 5843423
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NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 33.1%;
Best Local Similarity 61.1%;
Matches 11; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-243-545-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-993-962-2
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Pred. No. 4.7;
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1 Sequence 2, Application US/08243545

1 Sequence 2, Application US/08243545

1 Sequence 2, Application US/08243545

2 Sequence 2, Application US/08243545

2 GENERAL INFORMATION:

3 APPLICANT: Lyman, Stewart D.

4 APPLICANT: Beckmann, M. Patricia

7 TILE OF INVENTION:

8 CORRESPONDENCE ADDRESS:

9 CORRESPONDENCE ADDRESS:

1 CITY: Seattle

1 STREET: 51 University Street

1 CITY: Seattle

1 STREET: Bashington

1 CONDUTRY: US

2 ZIP: 98101

1 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

1 COMPUTER: Apple Macintosh

1 COMPUTER: Apple Macintosh

1 COMPUTER: Apple Macintosh

2 COMPUTER: Apple Macintosh

3 SOFTWARE: US/08/243,545

FILING DATE: 11-MAY-1994

5 FILING DATE: 11-MAY-1993

5 FILING DATE: 03-DEC-1993

5 FILING DATE: August 25, 1993

6 FILING DATE: August 25, 1993

6 FILING DATE: August 25, 1993

6 FILING DATE: August 25, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; PAGES: 1157-1167
; DATE: 1993
; RELEVANT RESIDUES IN SEQ ID NO: 7: FROM 1 TO 231
US-08-220-379B-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/220,379B
FILING DATE: 28-MAR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Haley 17, James F
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: 27,794
REPERENCE/DOCKET NUMBER: 212-596-9000
TELECHONE: 212-596-9000
TELECHONE: 212-596-9000
TELECHONE: 212-596-9000
TELECHONE: CHARACTERISTICS:
LENGTH: 231 annino acids
TYPE: annino acids
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/106,463
FILING DATE: August 12, 1993
FILING TATON: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 33.1%;
Best Local Similarity 61.1%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYPOTHETICAL: NO ANTI-SENSE: NO FRAGMENT TYPE: N-terminal PUBLICATION: ATTHORS: Lyman, et al. JOURNAL: Cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :||| | |:|||| ::||
192 LLELLEPLTLVLLAAAWG 209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide HYPOTHETICAL: NO
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Indels

Pred. No. 4.7;

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Best Local Similarity 61.1%; Pr
Matches 11; Conservative 4;
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192 LLLLLPLTLVLLAAAWG 209
                                                                      1 MLLLSLTLSLVLLGSSWG 18
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                                                                                                                                                                                                                                                                                                                                                                                                             Seattle
Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: De CLASSIFICATION:
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STATE:
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Patent No. 6190655
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCES: 8
CORRESPONDENCES: ADDRESS:
ADDRESSEE: Stephen L. Malaska, Immunex Corporation
STREET: 51 University Street
                                                                                                                                                                                                                                     Score 55; DB 2;
Pred. No. 4.7;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0.1
SOFTWARE: Microsoft Word, Version #5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PLIANG DATE:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/162,407
FILING DATE: December 3, 1993
APPLICATION NUMBER: US/111,758
FILING DATE: August 25, 1993
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/106,463
FILING DATE: August 12, 1993
ATTORNEY/ABORT: MAY 24, 1993
ATTORNEY/ABORT INFORMATION:
NAME: MAISKA, Stephen L.
REGISTRATION NUMBER: 32,655
RESERENGE/DOCKET UNBER: 32,655
RESERENGE/DOCKET UNBER: 2813-C
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 2665
TELEFAX: 2665) 233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/160,841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US/08/162,407
| TELEPHONE: (206) 587-0430
| TELEXA: (206) 233-0644
| TELEX: 756822
| INFORMATION FOR SEQ ID NO: 2:
| SEQUENCE CHARACTERISTICS:
| LENGTH: 231 amino acids
| TYPE: amino acid
| TYPE: amino acid
| TYPE: TOPCOLOGY: 11near
| MOLECULE TYPE: protein
| US-08-993-962-2
                                                                                                                                                                                                                                     Query Match 33.1%;
Best Local Similarity 61.1%;
Matches 11; Conservative
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192 LLLELLPLTLVELAAAWG 209
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amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 231 amino acida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 51 Univers
CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
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US-09-160-841-2
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33.1%; Score 55;

Query Match

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Length 231;
Sequence 2, Application PC/TUS9405365
GENERAL INFORMATION:
APPLICANT: Lyman, Stewart D.
APPLICANT: Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE: ADDRESS:
ADDRESSE: Stephen L. Malaska, Immunex Corporation
STREET: 51 University Street
                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05365
FILING DATE: May 24, 1994
CLASSIFICATION:
PRIOR APPLICATION NUMBER: -to be assigned-
FILING DATE: May 11, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33.1%; Score 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/209,502
FILING DATE: March 7, 1994
CLASSIFICATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/162,407
FILING DATE: December 3, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/111,758
FILING DATE: August 25, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/106,463
FILING DATE: August 12, 1993
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/068,394
FILING DATE: May 24, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (200,
TELEFAX: 756822
INFORMATION FOR SEQ. ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 231 amino acids
"VPE: amino acids
"VPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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DB 1; Length 268;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION NATA:
APPLICATION NATA:
APPLICATION UNMER: US/08/765,192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-765-192-2
Sequence 2, Application US/08765192
SEPPLICANT: Greene, John et al.
TITLE OF INVENTION: Human Elastase IV
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 55; DB Pred. No. 5.5; Mismatches
                                    ADDRESSEE: CARELLA, BYRNE, BAIN, GIL
ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
                                                                                                                                                                                                                                                                                 CUSTRAINT APPLICATION DATA:
APPLICATION NUMBER: US/08/270,584A
FILING DATE: July 5, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 LLSLTLSLVLLGSSWGCGVPAITPALS 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER REALABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFRERUCE/DOCKET NUMBER: 325,
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36,134
                                                                                                                                                                                                                                              OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 268 AMINO ACIDS
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 33.1 Best Local Similarity 40.7 Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                FILING DATE: July 5,
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: LINEAR; MOLECULE TYPE: PROTEIN US-08-270-584A-2
                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION: 435
  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MD
US
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STATE: MD
COUNTRY: US
ZIP: 20850
                                                                                                                                           COUNTRY: US
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0
                                                                                                                                                                                                   Sequence 6, Application PC/TUS9503866

GENERAL INFORMATION:
APPLICANT: CytoMed, Inc. (all states except US)
APPLICANT: CytoMed, Inc. (all states except US)
TITLE OF INVENTION: STABILIZED DIMER OF KIT LIGAND
TITLE OF INVENTION: FLT-3/FLK-2 LIGAND
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 5; Length 231;
                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03866
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    Pred. No. 4.7;
                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/220,379
FILING DATE: 28-MAR-1994
ATTORNEY AGENT INFORMATION:
NAME: Haley Jr, James F
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET
TELECOMMUNICATION INFORMATION:
TELEFRAN: 212-596-9090
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ET AL.
Human Elastase IV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08270584A Patent No. 5710035 GENERAL INFORMATION: BT AL. TITLE OF INVENTION: Human Elasta:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33.1%;
61.1%;
  61.18;
                                                                                      192 LLLLLLPLTLVLLAAAWG 209
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192 LLLLLPLTLVLLAAAWG 209
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                                                              1 MLLLSLTLSLVLLGSSWG 18
Best Local Similarity 61.1
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 33.1
Best Local Similarity 61.1
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: Protein LOCATION: 1..205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                             New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: Ur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
PCT-US95-03866-6
                                                                                                                                                                   RESULT 7
PCT-US95-03866-6
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Gaps

PF125US

REFERENCE/DOCKET NUMBER:

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FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Fusion gene of
OTHER INFORMATION: human protease F in CFEK2 zymogen vector
US-09-386-642-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Description of Artificial Sequence: Fusion gene; OTHER INFORMATION: with homo sapien serine protease catalytic domain US-09-386-642-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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Pred. No. 16;
3; Mismatches 8; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8; Indels
                                                                                                               APPLICANT: Darrow. Andrew
APPLICANT: Olivenson
APPLICANT: Adrade-Gordon, Patricia
TITLE OF INVENTION: Zymogen Activation System
FILE REFERENCE: ORT-1028
CURRENT APPLICATION NUMBER: US/09/386,642
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ. ID NOS: 60
SOFTWARE: Patentin Ver. 2.0
SEQ. ID NO S. 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31.3%; Score 52; DB 4; 50.0%; Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Darrow, Andrew
APPLICANT: Q1, Jenson
APPLICANT: Andrade-Gordon, Patricia
TITLE OF INVENTION: 2ymogen Activation System
FILE REFERENCE: ORT-1028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/386,642 UNRENT FILING DATE: 1999-08-31 NUMBER OF SEQ ID NOS: 60 SOFTWARE: PATENTIN VET. 2.0
                  RESULT 11
US-09-386-642-53
Sequence 53, Application US/09386642
Patent No. 6420157
GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-386-642-12; Sequence 12, Application US/09386642; Patent No. 6420157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/09110116
Patent No. 6013479
GENERAL INFORMATION:
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50.0%;
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APPLICANT: Cohan, Victoria L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 31.3°
Best Local Similarity 50.0°
Matches 11; Conservative
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Best Local Similarity
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US-09-110-116-4
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                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
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Pred. No. 5.5;
5; Mismatches 11; Indels
                                                                                                                                                                                                                                         33.1%; Score 55; DB 2; Length 268; 40.7%; Pred. No. 5.5;
                                                                                                                                                                                                                                                                               5; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/199,793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Greene, John et al.
TITLE OF INVENTION: Human Elastase IV
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                        3 LLSLTLSLVLLGSSWGCGVPAITPALS 29
                                                                                                                                                                                                                                                                                                                                             1 HIGITVLAALLACASSCGVPSFPPNLS 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/765,192
FILING DATE: Apr-24-97
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/09199793
Patent No. 6107075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF11;
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
                            INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 268 annino acids TYPE: amino acid
TELECOMMUNICATION INFORMATION:
TELEPHONE: 3013098504
TELEFAX: 3013098439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33.18;
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amino acid
                                                                                                                                                                                                                                                                               11; Conservative
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; MOLECULE TYPE: protein
US-09-199-793-2
                                                                                                                                          single
                                                                                                                                                           ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-765-192-2
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Matches 11; Conserva
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nes 11; Conserva
                                                                                                                                        STRANDEDNESS:
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20850
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Sequence 6, Application US/09296284A

Patent No. 6204040

GENERAL INFORMATION:
APPLICANT: Choi, Eui-Sung

APPLICANT: Lee, Eun-Hae

TITLE OF INVENTION: Gluconobacter Suboxydans Sorbitol Dehydrogenase, Genes

TITLE OF INVENTION: and Methods of Use Thereof

TITLE OF INVENTION: and Methods of Use Thereof

CURRENT APPLICANTON and Methods of Use Thereof

CURRENT PELICAND NUMBER: US/09/296,284A

SOFFWARE: PatentIn Ver. 2.0

SEQ ID NO 6

LENGTH: 306
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APPLICANT: Rhee, Sang-Ki
APPLICANT: Rhee, Sang-Ki
APPLICANT: Lee, Eun-Hae
TITLE OF INVENTION: Gluconobacter Suboxydans Sorbitol Dehydrogenase, Genes
TITLE OF INVENTION: and Methods of Use Thereof
FILE REFERENCE: 1533.0870000
CURRENT APPLICATION NUMBER: US/09/296,284A
CURRENT FILING DATE: 1999-04-22
NUMBER OF SEO ID NOS: 87
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                                                                                                                                                                                                                                                                                                                                                                              Score 50; DB 3; Length 344;
Pred. No. 35;
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                                                                                                                                                                                                                                                                                                                                                                                                                             4; Mismatches 13; Indels
              TITLE OF INVENTION: HUMAN EMRI-LIKE G PROTEIN COUPLED TITLE OF INVENTION: RECEPTOR FILE REPERENCE: PF-0550 US CURRENT APPLICATION NUMBER: US/09/110,116 CURRENT FILING DATE: 1998-07-02 NUMBER OF SEQ ID NOS: 4 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 4 LENGTH: 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 48.5; DE
Pred. No. 44;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       250 MLAFKATAQLFILGCTWCLGILQVGPA 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MLLLSLTLSLVLLGSSWGCGVPAITPA 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-296-284-27
; Sequence 27, Application US/09296284A
; Patent No. 6.204040
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                          CRGANISM: HOMO SAPIENS
FEATURE:
COTHER INFORMATION: 2935597, Genbank
US-09-110-116-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Gluconobacter suboxydans
US-09-296-284-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 LTLSLVL-LGSSWGCGVPAITP 26
                                                                                                                                                                                                                                                                                                                                                                           Query Match 30.1%;
Best Local Similarity 37.0%;
Matches 10; Conservative
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Best Local Similarity 45.5%;
Matches 10; Conservative
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APPLICANT: Stuart, Susan G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 27
LENGTH: 280
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                                                                                                                                                                                                                                   TYPE: PRT
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                                           Score 48.5; DB 4; Length 306; Pred. No. 48;
                                                                           Indels
                                                                          8;
                                                                           Mismatches
                                                                                                                                                                                   Search completed: December 20, 2002, 15:20:38 Job time: 2.86957 secs
; ORGANISM: Gluconobacter suboxydans US-09-296-284-6
                                                                                                                             269 IRLALALARKWGAGVPKVLP 290
                                                                                                        6 LTLSLVL-LGSSWGCGVPAITP 26
                                             29.2%;
                                             Query Match
Best Local Similarity 45.55
Matches 10; Conservative
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December 20, 2002, 15:12:13 ; Search time 5.08696 Seconds (without alignments) 864.421 Million cell updates/sec
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                      166
1 MLLLSLTLSLVLLGSSWGCGVPAITPALSYNQR 33
                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                           908470 segs, 133250620 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                             - protein search, using sw model
                                                                                                                                                                                                   US-09-856-319B-4_COPY_1_33
                                                                                                                                                                                                                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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/SIDS2/gcgdata/geneseq/genesegp-embl/AA1990.DAT:* /SIDS2/gcgdata/geneseq/geneseqp-embl/Aa1993.DAT:* /SIDS2/gcgdata/geneseq/geneseq-embl/AA1994.DAT:* /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1995.DAT:* /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1995.DAT:* /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:* /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1989.DAT: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1992.DAT: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:* /SIDS2/gcgdata/geneseq/genesegp-emb1/AA1999.DAT /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2000.DAT /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2001.DAT: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2002.DAT: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1998 /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1991 /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1997

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result			8 Query	!		
ON .	score		Length	g :	ID	Description
н	166	100.0	264	21	AAB11711	Mouse serine prote
7	150	90.4	264	21	.AAB11710	Human serine prote
e	133	80.1	192	21	AAB54077	Human pancreatic c
4	68	41.0	44	21	AAY64742	Human 5' EST relat
ស	68	41.0	263	23	AAU82738	Amino acid sequenc
9	67	40.4	146	21	AAB54191	Human pancreatic c
7	59	35.5	195	20	AAY11649	Human 5' EST secre
80	58	34.9	306	23	AAU95588	Human olfactory an
6	58	34.9	312	22	AAG71664	Human olfactory re
10	58	34.9	312	22	AAG72192	Human olfactory re

Serine proteases BSSP5, useful in detecting homologs, mutants and

N-PSDB; AAA61734.

Human OR-11ke poly Drosophila melanog Drosophila melanog Human 5' EST secre Mouse flt-3 ligand Murine flt3-1igand Mouse Flt-3 ligand	Fil-3 MoT110 Fit-3 nella t caldec caldec elasta phi1-a	prometrical properties of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the	Human secreted pro- Human polypeptide Human protein sequ Herbicidally activ Human ORFX ORF1716 Drosophila melanog Human prostate tum Rat camello 1 (Rcm Human cell surface Novel human diagno Human mature EGF-1 Human mcture EGF-1 Human EGF-1 Human EGF-1
AAG72355 AAB07181 ABB60694 AAX11650 AAK67540 AAW67768	AAR66177 AAB20189 AAU38137 AAR80683 AAR88481 AAY31895	AAB66394 AAB67538 AAB67539 AAB67544 AAB67541 AAB67541 AAB67541	AAV41332 AAB90142 AAB39014 ABB91392 AAB41952 AAB473942 AAR139992 AAE13609 AAE13609 AAE13609 AAE13609
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## ALIGNMENTS

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BSSP5; serine protease; human; hBSSP5; mouse; mBSSP5; brain; diagnostic marker; antibody; transgentc animal; Alzheimer's disease; epilepsy; cancer; inflammation; infertility; pancreatitis; prostatic hypertrophy.
                                                                                                                                                                                                                                                                  Mitsui
                                                                           Mouse serine protease BSSP5 (mBSSP5) SEQ ID NO:4.
                                                                                                                                                                                                                                                                  Yamaguchi N,
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                                                                                                                                                                                                                                                                 Α,
                AAB11711 standard; Protein; 264
                                                                                                                                                                                                                                                                  Kominami
                                                                                                                                                                                                        99WO-JP06473
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                                                                                                                                                                                                                                              (FUSO ) FUSO PHARM IND LTD.
                                                        23-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                     WPI; 2000-400058/34
                                                                                                                                                                                                                                                                 Uemura H, Okui A,
                                                                                                                                                                WO200031243-A1.
                                                                                                                                                                                                      19-NOV-1999;
                                                                                                                                                                                                                          20-NOV-1998;
                                                                                                                                                                                    02-JUN-2000.
                                     AAB11711;
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RESULT 1
          AAB11711
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The invention relates to novel serine proteases designated BSSP5

(AAB11710-B11711), and to nucleic acids encoding them (AAA61731-A61734).
The invention also relates to vectors and transformants comprising BSSP5
nucleic acids; transgenic animals in which the expression level of BSSP5
can be varied; and an mBSSP5 knockout mouse. The invention additionally
cancipasses anti-BSSP5 antibodies and methods of production of such
antibodies, methods of BSSP5 detection using the antibodies, and the
cuse of BSSP5 proteins or fragments as diagnostic markers for certain
medical conditions, e.g., pencreatitis A method for detecting
pancreatitis comprising measuring BSSP5 concentration in the blood or
urine, and a pancreatitis diagnostic agent containing an anti-BSSP5
antibody is also disclosed. Nucleotides encoding BSSP5 were initially
solated in a human brain cDNA library using degenerate PCR primers
(AAA61744-A61745) based on conserved regions of serine proteases. The
BSSP5 serine proteases and nucleotides encoding them are useful in
BSSP5 serine proteases and nucleotides encoding them are useful in
samples (e.g., blood, union, brain, prostate gland, placenta, testis,
pancreas and spleen) as diagnostic markers for conditions such as
pancreas and spleen) as diagnostic markers for conditions such as
conditions and prostatic hypertrophy. Sequence AAB11710 represents
conserved.
Chuman BSSP5 (hBSSP5), and sequence AAB11711 represents murine BSSP5
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polymorphic variants as markers for diagnosis of e.g. Alzheimer's disease, epilepsy, cancer and inflammation, using blood, urine, pancreas or other tissues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human serine protease BSSP5 (hBSSP5) SEQ ID NO:2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 166; DB 21 100.0%; Pred. No. 1e-13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MLLLSLTLSLVLLGSSWGCGVPAITPALSYNQR 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MLLLSLTLSLVLLGSSWGCGVPAITPALSYNQR 33
                                                                                Claim 3; Page 55-56; 70pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB11710 standard; Protein; 264 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Uemura H, Okui A, Kominami K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98JP-0347806.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-400058/34.
N-PSDB; AAA61733.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (mBSSP5).
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Serine proteases BSSP5, useful in detecting homologs, mutants and

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The invention relates to novel serine proteases designated BSSP5

(AABI1710-B11711), and to nucleic acids encoding them (AAA61733-A61734).

The invention also relates to vectors and transformants comprising BSSP5

nucleic acids; transgenic animals in which the expression level of BSSP5

can be varied; and an mBSSP5 knockout mouse. The invention additionally

encompasses anti-BSSP5 antibodies and methods of production of such

antibodies, methods of BSSP5 detection using the antibodies, and the

cuse of BSSP5 proteins or fragments as diagnostic markers for certain

antibodial conditions, e.g., pancreatitis. A method for detecting

pancreatitis comprising measuring BSSP5 concentration in the blood or

urine, and a pancreatitis diagnostic agent containing an anti-BSSP5

antibody is also disclosed. Nucleotides encoding BSSP5 were initially
isolated in a human brain cDNA library using degenerate PCR primers

(AAA61744-A61745) based on conserved regions of serine proteases. The
BSSP5 serine proteases and nucleotides encoding them are useful in
detecting homologues, mutants and polymorphic variants in biological
samples (e.g., blood, urine, brain, prostate gland, placenta, testis,
pancreas and spleen) as diagnostic markers for conditions such as
Alzheimer's disease, epilepsy, cancer, inflammation, infertility,
chuman BSSP5 (BBSSP5), and sequence AABI1711 represents murine BSSP5

contracts and prostatic hypertrophy. Sequence AABI1711 represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    detection; diagnosis; identification; cytostatic; neuroprofective; nootropic; immunomodulatory; relaxant; contraceptive; gynaecological; antiinflammatory; cardiant; gene therapy; chromosome mapping; linkage analysis; tissue identification; tissue typing; forensic; neural; immune system; muscular; reproductive; gastrointestinal; pulmonary; cardiovascular; renal; proliferative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
polymorphic variants as markers for diagnosis of e.g. Alzheimer's disease, epilepsy, cancer and inflammation, using blood, urine, pancreas or other tissues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human pancreatic cancer antigen protein sequence SEQ ID NO:529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; pancreas; pancreatic cancer; pancreatic cancer antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 264;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 90.4%; Score 150; DB 21;
Best Local Similarity 87.9%; Pred. No. 1.3e-11;
Matches 29; Conservative 3; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MILLSLTLSLVLLGSSWGCGVPAITPALSYNQR 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MLLLSLTLSLVLLGSSWGCGIPAIKPALSFSQR 33
                                                                                        Claim 1; Page 51-52; 70pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB54077 standard; Protein; 192 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-MAR-2000; 2000WO-US05989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-MAR-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           264 AA;
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N-PSDB; AAZ42356
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                      proteins, called pancreatic cancer antigens, given in AAB54008 to proteins, called pancreatic cancer antigens have cytostatic.

TAAB54466. The human pancreatic cancer antigens have cytostatic.

Chapter human pancreatic cancer antigens have cytostatic.

Chapter herapy the polynculectide and proteins can be used for an gene therapy. The polynculectide and proteins can be used for preventing, treating, or ameliorating a medical condition or in assays for diagnosing a pathological condition or a susceptibility to one in a cubject. Binding partners to the proteins and the activity of the proteins and the activity of the carcer is an be identified. The pancreatic cancer antigens can be used to detect, treat or prevent pancreatic disorders, especially cancer.

Concept and antagonists to the antigens can be screened for. The pancreatic cancer antigen polynucleotides can be used to design nucleic acid hybridisation probes that can be used in chromosome mapping, linkage can allysis, tissue identification and/or typing and a variety of forensic and diagnostic methods. The proteins can be used to generate antibodies which are used to purify, detect and target the polypeptides, including conteins can be used to generate antibodies both in vivo and in vitro diagnostic and therapeutic methods. The proteins can be used to generate antibodies conteins can be used to treat or prevent neural, immune system, muscular, represent content of the proteins can adjoin the and margal to an antibodies of proliferative disorders. AAG992221 to AAG99240 candiovascular, represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                         New nucleic acid that is a pancreatic cancer antigen for preventing, treating, or ameliorating a medical condition, particular pancreatic cancer, or for use in assays for diagnosing a pathological condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; 5' EST; expressed sequence tag; secreted protein; diagnosis; gene therapy; chromosome mapping; upstream regulatory sequence; forensic; location; development; protein synthesis; stability; regulation; identification.
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                                                                                                                                                                                                                                                                                                                                                                                                                sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80.1%; Score 133; DB 21; Length 192; 86.2%; Pred. No. 1.5e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human 5' EST related polypeptide SEQ ID NO:903.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 SLTLSLVLLGSSWGCGIPAIKPALSFSQR 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SLTLSLVLLGSSWGCGVPAITPALSYNQR 33
                                                                                 Claim 11; Page 966; 1379pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dumas Milne Edwards J, Duclert A,
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98US-0069047
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Best Local Similarity 86.2%
Matches 25; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                            192 AA;
N-PSDB; AAC98842.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Sednence
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sequences, corresponding to human secreted proteins. AAY6651 to
AAY65438 represent the EST-related proteins corresponding to AAZ4265 to
AAX4655. The S. ESTs can be used for producing secreted human gene
products. They can be used for producing secreted human gene
products. They can be used for producing secreted human gene
cejons (UTRs) and upstream regulatory regions which control the
coation, development stage, rate, and quantity of protein synthesis, well as stability of mRNA. The ESTs are also useful as probes for chromosome mapping, and to obtain full length cDNA clones. The ESTs can also be used in forenist procedures to identify individuals, or in diagnostic procedures to identify individuals having genetic diseases resulting from abnormal gene expression. The products may also be used in coating expression. The products may also be used in customers to identify individuals having senetic diseases resulting from abnormal gene expression. The products may also be used in customer expression actids encoding signal peptides can be used for directing extracellular secretion of a polypeptide into a membrane, or importing a polypeptide into a cell. The proteins encoded by the EST sequences may be useful in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; protease; cancer; immune-related disorder; cardiovascular disease; neuronal-associated disease; metabolic disorder; inflammatory disorder; nervous system disorder; sexual dysfunction; pain; mood disorder; hypertension; psychotic disorder; neurological disorder; dyskinesia; viral infection; human immunodeficiency virus; HIV; non-viral infection; ocular disease; cytostatic; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    treating a variety of human conditions. Secreted proteins have therapeutic value, and the identification of new secreted proteins is valuable. AAZ42249 to AAZ42264 and AAY64644 to AAX46265 represent
                                           diagnostic, forensic, gene therapy, and chromosome mapping procedures
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                                                                                                                                                                                                  AAZ42265 to AAZ43075 represent, novel 5' expressed sequence tag (EST)
Novel secreted protein 5' expressed sequence tag sequences used in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41.0%; Score 68; DB 21; Length 44; 45.5%; Pred. No. 0.092;
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                                                                                                                    Claim 3; Page 629; 837pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44 AA;
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The present invention relates to the isolation of novel human proteases, and the nucleic acids encoding them. The sequences of the invention are useful for treating diseases and disorders such as cancers (e.g. breast, colon, lung), immune-related diseases and disorders (e.g. inflammatory diseases and asthma), cardiovascular diseases (e.g. restenosis and coronary thrombosis), brain or neuronal-associated diseases, metabolic disorders (e.g. diabetes, obesity), inflammatory disorders (e.g. rheumatoid arthritis and positasis), central or peripheral nervous system diseases, migraines, pain, sexual dysfunction, modisorders, attention disorders, hypotension, hypertension, psychotic disorders, neurological disorders. hypotension, hypertension, psychotic disorders, neurological disorders. Che nucleic acids and polypeptides are also useful for treating viral infections caused by human immunodeficiency virus (HIV), and non-viral infections such as ocular disease (e.g. glaucoma) and macular cheases of cheases.
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                                  Nucleic acids encoding novel human proteases, useful for useful for treating diseases and disorders such as cancers, immune-related diseases and disorders, cardiovascular disease (e.g. restenosis) and inflammatory disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch 41.0%; Score 68; DB 23; Length 263; 1 Similarity 51.7%; Pred. No. 0.63; 15; Conservative 4; Mismatches 10; Indels
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                                                                                                                                                                                                                        Claim 6; Fig 2M; 313pp; English.
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N-PSDB; AAC98956.
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upstream regulatory sequence; cytokine activity; cell proliferation;
differentiation; haematopolesis regulation; tissue growth regulation;
reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
treating, or ameliorating a medical condition, particular pancreatic cancer, or for use in assays for diagnosing a pathological condition
                                                                                                                                 to AAC99231 encode the human pancreatic cancer associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; secreted protein; EST; expressed sequence tag; diagnosis;
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                                                                             English.
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                                                                                Claim 11; Page 1081; 1379pp;
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les 12; Conserv
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anxiety and schizophrenia
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                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                             306 AA;
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                                                                        human secreted proteins, and encode the proteins given in AAX10531 to human secreted proteins, and encode the proteins given in AAX11533 to human secreted proteins, and encode the proteins given in AAX11533 to AAX11679, respectively. The proteins given represent the signal peptide and an N-terminal fragment of a secreted protein. The nucleic acid sequences can be used for producing secreted human gene products. They can also be used for producing secreted human gene products. They proteins obtained may have cytokine activity, call proliferation/differentiation activity, haematopoies is requiating activity, tissue growth regulating activity, reproductive hormone regulating activity, encoductive hormone regulating activity, chemotactic/ chemokinetic activity, haemostatic activity, exceptor/ ligand activity, anti-inflammatory activity, tumour inhibition activity or other activities. The products can be used in forensic, gene therapy and chromosome mapping promoter sequences. The nucleic acids encoding the signal peptide can be used for directing aximal peptide can be used for directing aximal peptide into a membrane, or importing a polypeptide into a cell.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GPCR; tranquilizer; antidepressant; neuroleptic; endocrine; anabolic; anorectic; taste; fragrance; food additive; cosmetic; cell migration; sterility; psychotic disorder; neurological disorder; anxiety; schizophrenia; manic depression; depression; axonal growth; menstrual cycle; appetite sexual motivation; sexual attraction;
                                                                                                                                                                                                                                                                                                                                                                             Gaps
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New nucleic acids encoding human secreted proteins - obtained from CDNA libraries derived from liver, lung, large intestine, colon,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human olfactory and pheromone G protein-coupled receptor #75.
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                                                                                                                                                                                                                                                                                                                                                 Length 195;
                                                                                                                                                                                                                                                                                                                                               Score 59; DB 20; Length 19
Pred. No. 6.8;
5; Mismatches 10; Indels
                                                     Claim 27; Page 378-379; 398pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                        3 LLSLTLSLVLLGSSWGCGVPAITPALS 29
                                                                                                                                                                                                                                                                                                                                                                                                                       AAU95588 standard; Protein; 306 AA
                                                                                                                                                                                                                                                                                                                                                 35.5%;
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                           thyroid and pancreas tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                               Query Match 35.55
Best Local Similarity 44.44
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                       195 AA;
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The inversion tractory and free control of the GPCR, a specific active portion and its encoding polynuclectide. Also included are an agonist, antagonist or inhibitor of the GPCR or the polynuclectide, a cell transformed by the vector, a non-thuman mammal comprising a partial or total deletion of the polynuclectide encoding the receptor and screening (detection and possibly, recovering) of compounds which are known or not known to be agonist, antagonists or inhibitors of natural compounds to the GPCR. The receptor-derived agonists, antagonists, inhibitors or compounds are used as an agonists, inhibitors or compounds are used as an event in provement, elimination or substitution of an existing taste and/or a tragrance of (or in) the food and/or cosmetic products. They can also be used in the preparation of medicament in the treatment and/or prevention of a mammalian disorder, such as cell migration, sterility, psychotic and neurological disorders, including anxiety, schizophrenia, manic depression, depression, for promoting axonal growth, nerve cell connection and nerve regeneration for modulating maile and female
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               behaviours, such as stimulation or suppression of appetite, sexual motivation, sexual attraction, aggression and for promoting or suppressing chemical communication between organisms. The present
                                                                                 The invention relates to olfactory and Pheromone G-protein coupled
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Pred. No. 15;
2; Mismatches 6; Indels
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Disclosure; Page 238-239; 833pp; English.
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(YEDA ) YEDA RES & DEV CO LTD.
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60.0%;
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24-FEB-2000; 2000US-0184809.
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AAG72355;
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                                one of a number of novel polynucleotides. The polynucleotides can be used in screening for olfactory agonists and antagonists. The methods allow for the determination of primary scents and the identification of the odour receptors used to detect these primary scents. The methods also enable determination of secondary scents and the identification of combinations of odour receptors that are involved in detecting such secondary scents. This enables the construction of a scent representation of calso called a scent fingerprint or scent profile), which may be used to re-create and edit scents. Libraries of olfactory receptors are useful for determining the interaction pattern of a composition with the receptors, and can be used for determining differences in the olfactory (x)
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Pred. No. 15;
2; Mismatches 6; Indels
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               Claim 11; Page 830-831; 1857pp; English.
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(YEDA ) YEDA RES & DEV CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              133 LLLSHRVCLQLAGSAWACGV 152
                                                                                                                                                                                                                                                                                                                                                    34.9%;
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2000US-0184809.
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Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                    312 AA;
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24-FEB-2000;
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                                                                                                                                                                                                                                                                                                                    Sequence
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The present sequence is a polypeptide encoded by one of 344 newly mined human genes. It was used as a query sequence in a database search of chuman genes. It was used as a query sequence in a database search of chiactory receptor (OR) like sequences. The invention relates to isolated polymucleotides encoding polypeptides involved in olfactory sensation. The polymucleotides can be used in screening for olfactory agonists and antagonists. The methods allow for the determination of primary scents and the identification of the odour receptors used to detect these primary scents. The methods also enable determination of secondary scents and the identification of combinations of odour receptors that are involved in detecting such secondary scents. This enables the construction of a scent representation (also called a scent fingerprint or scent profile), which may be used to re-create and edit scents. Libraries of olfactory receptors are useful for determining the interaction pattern of a composition with the receptors, and can be individuals.
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(also called a scent fingerprint or scent profile), which may be used to re-create and edit scents. Libraries of olfactory receptors are useful for determining the interaction pattern of a composition with the receptors, and can be used for determining differences in the olfactory faculties of different individuals.
                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; olfactory receptor; OR; primary scent determination; secondary scent determination; polypeptide library; odour receptor; scent profile; scent fingerprint; scent representation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New polynucleotides which encode polypeptides involved in olfactory
                                                                                                                                                                                                                                                                                                                                                              ;
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                                                                                                                                                                                                                                                                                            Length 312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human OR-like polypeptide query sequence, SEQ ID NO: 2036.
                                                                                                                                                                                                                                                                                                                                                              6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fuchs T,
                                                                                                                                                                                                                                                                                        DB 22;
15;
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                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                        34.9%; Score 58; 60.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 6; Page 1364; 1857pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAG72355 standard; Protein; 312 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Smith D, Lancet D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (YEDA ) YEDA RES & DEV CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    133 LLLSHRVCLQLAGSAWACGV 152
                                                                                                                                                                                                                                                                                                                                                                                                                                    2 LLLSLTLSLVLLGSSWGCGV 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0158615
2000US-0184809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 60.0
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-290713/30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (DIGI-) DIGISCENTS.
                                                                                                                                                                                                                         312 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200127158-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bellenson J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-OCT-1999;
24-FEB-2000;
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312 AA;

Query Match

Best Loca Matches

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AAB07181;

RESULT 12 AAB07181

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The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; secreted protein; EST; expressed sequence tag; diagnosis; forensic; gene therapy; chromosome mapping; signal peptide; upstream regulatory sequence; cytokine activity; cell proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                   developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 441;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 8874; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                          Drosophila melanogaster polypeptide SEQ ID NO 8874.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human 5' EST secreted protein SEQ ID NO:302.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33.4%; Score 55.5; 48.3%; Pred. No. 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                210 LLLSLTV-LPNVNSSWYYDAPSIAPSLDF 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 LLLSLTLSLVLLGSSWGCGVPAITPALSY 30
                                            ABB60694 standard; Protein; 441 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY11650 standard; Protein; 123 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Li PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                                                                                                                                                                                                                                                  23-MAR-2001; 2001WO-US09231
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                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                    Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ABB57737-ABB72072).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-656860/75.
N-PSDB; ABL04797.
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Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          441 AA;
                                                                                                                                                                                                                                                                                                                               WO200171042-A2
                                                                                                                                                                                                                                            pharmaceutical
                                                                                                                                26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                         27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seguence
                                                                                       ABB60694;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY11650;
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  RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY11650
                        4BB6069
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is the protein sequence for the Drosophila melanogaster imaginal disc growth factor 3 (IDGF3). The sequence encoding this protein was used to isolate the IDGF4 cooling sequence. IDGF4 is a member of the chitinase related proteins (CHRP) and is involved in the promotion of cell growth, motility and morphogenesis. The gene and promotion of cell growth, motility and morphogenesis. The gene and promoted to have mammalian homologues. They can be used in the treatment of cancer, wound healing, tissue regeneration following arthritis, osteoporosis, other skeletal disorders and burns, for evitalising scar tissue resulting from surgical procedures, irradiation, laceration, toxic chemicals, viral or bacterial infection or burns, to promote tissue growth during tissue engineering, for example tissues for skin graft replacements and bone regrowth, and to modulate the function of the female reproductive tract. In addition, they can also be used to increase meat, egg, sperm and milk production in animals. One possible method of use is by gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New imaginal disc growth factor polypeptide, useful for healing wounds, promoting tissue growth, modulating female reproductive tract functions and treating cell proliferative disorders such as cancer and metastasis
                                                                                                                                                                                                                                                                                                                                                                                                             Imaginal disc growth factor 3; IDGF3; chitinase related protein; CHRP; tissue growth; wound healing; bone repair; cartilage repair; angiogenesis; meat production; milk production; cancer; gene therapy.
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                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
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DB 22; Length 312;
15;
                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster imaginal disc growth factor 3.
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                                          2; Mismatches
34.9%; Score 58;
60.0%; Pred. No.
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                                                                                                                                                                                                                                     AAB07181 standard; Protein; 441 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 4; 40pp; English.
                                                                                                              133 LLLSHRVCLQLAGSAWACGV 152
                                                                                   2 LLLSLTLSLVLLGSSWGCGV 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98US-0052778.
                                                                                                                                                                                                                                                                                                                          (first entry)
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les 14; Conservative
                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bryant PJ, Kawamura K;
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                    Local Similarity
les 12; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-MAR-1998;
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Gaps

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Sequence Query Match

Best Loca Matches

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Domain
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                                                                                                                                                                                                                                                                                                                                                                       human secreted proteins, and encode the proteins given in AAY11533 to human secreted proteins, and encode the proteins given in AAY11533 to AAY11679, respectively. The proteins given represent the signal peptide and an N-terminal fragment of a secreted protein. The nucleic acid sequences can be used for producing secreted human gene products. They can also be used to develop products for diagnosis and therapy. The proteins obtained may have crytokine activity, cell proteins obtained may have crytokine activity, cell proteins obtained may have crytokine activity, reproductive hormone regulating activity, tissue growth regulating activity, haematopoiesis regulating activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, tumour inhibition activity on other activities. The products can be used in forensic, gene therapy and chromosome mapping procedures. The sequences can also be used for obtaining corresponding promoter sequences. The nucleic acids encoding the signal peptide can be used for directing extracellular secretion of a polypeptide or the insertion of a polypeptide into a membrane, or importing a polypeptide into a cell.
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differentiation; haematopoiesis regulation; tissue growth regulation; reproductive hormone regulation; chemotactic; chemokinetic; haemostatic; thrombolytic; anti-inflammatory; tumour inhibition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                           New nucleic acids encoding human secreted proteins - obtained from cDNA libraries derived from liver, lung, large intestine, colon, thyroid and pancreas tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 55; DB 20; Length 123; Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Flt-3 ligand; flt3-L; anemia; cancer; AIDS; gene therapy.
                                                                                                                                                                                                                          Lacroix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5; Mismatches
                                                                                                                                                                                                                                                                                                                                                Claim 27; Page 379-380; 398pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 LLSLTLSLVLLGSSWGCGVPAITPALS 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :|:|: || : ||||: ||||: || || 1 MLGITVLAALLACASSCGVPSFPPNLS 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= Sig_peptide
                                                                                                                                                                                                                         Duclert A, Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR67540 standard; Protein; 231 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 33.1%;
Best Local Similarity 40.7%;
Matches 11; Conservative
                                                                                                                                          98WO-IB01233
                                                                                                                                                                  97US-0904468
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N-PSDB; AAX40368.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse flt-3 ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               123 AA;
                                                                                                                                                                                               (GEST ) GENSET
                                                                                                                                          31-JUL-1998;
                                                                                                                                                                    01-AUG-1997;
                                                         Homo sapiens
                                                                                   409906439-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-AUG-1995
                                                                                                              11-FEB-1999
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Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA encoding mouse flt3-ligand (flt3-L) was isolated from a cDNA library of T-cell line PTB-0.344 in CV-1/EBNA-1 cells using a slide autoradiography method. Flt3-L stimulates production of progenitor and stem cells, and can be used e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 16; Length 231; 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated ligands for flt 3 receptors - useful for treating anaemia, AIDS and various cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3,
28..188
/label= Extracellular_domain
189..211
                                                     /label= Transmembrane_domain
212..231
/label= Cytoplasmic_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 55; DB 1
Pred. No. 27;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search completed: December 20, 2002, 15:16:42 Job time : 6.08696 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 25-27; 33pp; English.
                                                                                                                                                                                                                                                                   93US-0106463.
93US-0111758.
93US-0162407.
94US-0209502.
94US-0243545.
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61.1%;
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                                                                                                                                                                                                                                                   93US-0068394
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192 LLLLLEPLTLVLLAAAWG 209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in gene therapy protocols.
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Best Local Similarity 61.1'
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                             Beckmann MP, Lyman SD;
                                                                                                                                                                                                                                                                                                                                                                                       (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1995-008071/02.
N-PSDB; AAQ79076.
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                                                                                                                                                                                                                                                                   12-AUG-1993;
25-AUG-1993;
03-DEC-1993;
07-MAR-1994;
11-MAY-1994;
                                                                                                                                                                                                               19-MAY-1994;
                                                                                                                                                                                                                                                   24-MAY-1993
                                                                                                                                                                         07-DEC-1994
                                                                                                                                 EP627487-A.
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                                       Domain
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